

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: August 10, 2005, 05:00:04 ; Search time 3121 Seconds
(without alignments)
3063.017 Million cell updates/sec
US-10-660-763-2
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 21966066 seqs, 6356167942 residues
Total number of hits satisfying chosen parameters: 43932132
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3783.5	97.5	6609	8	US-10-302-689A-149442	Sequence 149442,
2	2405	62.0	6055	8	US-10-302-689A-149441	Sequence 149441,
3	1850	47.7	2947	1	PCT-US05-00517-3524	Sequence 3524, Ap
4	1654	42.6	1400	19	US-11-060-756-796	Sequence 796, App
5	1654	42.6	1400	19	US-11-060-756-5068	Sequence 5068, Ap
6	1206.5	31.1	3369	22	US-11-097-143-18926	Sequence 18926, A
7	1074.5	27.7	1183	22	US-11-136-527-3335	Sequence 3335, Ap
8	1074.5	27.7	1183	22	US-11-136-527-7431	Sequence 7431, Ap
9	1057	27.2	600	19	US-11-060-756-3332	Sequence 3332, Ap
10	1057	27.2	600	19	US-11-060-756-3333	Sequence 3333, Ap
11	1057	27.2	600	19	US-11-060-756-7604	Sequence 7604, Ap
12	1057	27.2	600	19	US-11-060-756-7605	Sequence 7605, Ap
13	1017	26.2	638	23	US-60-680-544-39317	Sequence 39317, A
14	1017	26.2	638	23	US-60-680-473-39317	Sequence 39317, A
15	1013	26.1	3198	22	US-11-097-143-24845	Sequence 24845, A
16	913.5	23.5	1433	23	US-60-669-241-2794	Sequence 2794, Ap
17	833	21.5	699	22	US-11-136-527-1734	Sequence 1734, Ap
18	792	20.4	657	23	US-60-680-544-17507	Sequence 17507, A
19	792	20.4	657	23	US-60-680-473-17507	Sequence 17507, A
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21	753.5	19.4	28918	22	US-11-097-143-18925	Sequence 18925, A
22	740	19.1	798	23	US-60-680-544-19988	Sequence 19988, A
23	740	19.1	798	23	US-60-680-473-19988	Sequence 19988, A
24	666.5	17.2	6021	18	US-11-191-644-13	Sequence 13, Appl
25	664	17.1	600	22	US-11-136-527-5830	Sequence 5830, Ap
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29	624.5	16.1	3840	22	US-11-012-067-9	Sequence 9, Appli
30	624.5	16.1	5434	13	US-10-940-774A-927	Sequence 927, App
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35	622	16.0	5763	13	US-10-940-774A-3759	Sequence 3759, Ap
36	618.5	15.9	4221	18	US-11-191-644-17	Sequence 17, Appl
37	617.5	15.9	5436	23	US-60-659-397-590	Sequence 590, App
38	617.5	15.9	5763	23	US-60-659-397-589	Sequence 589, App
39	609.5	15.7	1937	22	US-11-015-730-19	Sequence 19, Appl
40	609.5	15.7	2293	22	US-11-097-143-122	Sequence 122, App
41	609.5	15.7	2422	22	US-11-097-143-122	Sequence 36930, A
42	607.5	15.7	3849	18	US-11-191-644-3	Sequence 3, Appli
43	605.5	15.6	1933	2	PCT-US04-23309-10	Sequence 10, Appl
44	605.5	15.6	2104	2	PCT-US04-23309-9	Sequence 9, Appli
45	605.5	15.6	2183	2	PCT-US04-23309-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-10-302-689A-149442
; Sequence 149442, Application US/10302689A
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Asundi, Vinod
; APPLICANT: Ballinger, Dennis
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Liu, Jin
; APPLICANT: Loeb, Deborah
; APPLICANT: Montgomery, Julia, R.
; APPLICANT: Pace, Ann M.
; APPLICANT: Sheridan, James P.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 502CIP
; CURRENT APPLICATION NUMBER: US/10/302,689A
; CURRENT FILING DATE: 2002-11-22


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Db 1741 TTGGGTGAGCAGATTGGACGGGTTCCCCAGCGAGGGTCAAACTCCAGAGAGCTGGGTG 1800
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; Sequence 149441, Application US/10302689A
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Asundi, Vinod
; APPLICANT: Ballinger, Dennis
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Liu, Jin
; APPLICANT: Loeb, Deborah
; APPLICANT: Montgomery, Julia, R.
; APPLICANT: Pace, Ann M.
; APPLICANT: Sheridan, James P.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 502CIP
; CURRENT APPLICATION NUMBER: US/10/302,689A
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: 10/273,573
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 10/084,643
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/989,660
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 10/014,487
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: 09/952,981
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/905,059
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/898,888
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/919,002
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/770,160
; PRIOR FILING DATE: 2001-01-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 158931
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 149441
; LENGTH: 6055
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-302-689A-149441

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Qy 284 LeuLeuGluGlyGluProLeuGluProGlyGluLeuGlnLeuAenGluLeuThrVal 303
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Db	539	CGGCTGCAGCTCATTCGGAGGTGCAGAGCCCTGATGAGCAGCTGTGTACCATGGG	598	Db	1619	GCCTGCTACTCTCCGAAAGCGAGCTGTGGAGCTTTGGCATCTTGGCTCTGGGAGACCTTC	1678
QY	440	-----	440	QY	685	SerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnThrArgGluPheValGlu	704
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QY	440	-----	440	QY	705	LysGlyGlyArgLeuProCysProGluLeuCysProAspAlaValPheArgLeuMetGlu	724
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QY	440	-----	440	QY	725	GlnCysTyrAlaTyrGluProGlyGlnArgProSerPheSerThrIleTyrGlnGluLeu	744
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Db	959	CAGATTGGACGGTTCCTCCAGCAGGGGTCAAACCTCCAGAGAGCCTGGGTGAGGGGTCCG	1018	; TITLE OF INVENTION: METHODS OF USING DATABASES TO CREATE GENE-EXPRESSION MICROARRAYS,			
QY	499	-----	499	; FILE REFERENCE: 18525-04130			
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QY	505	ValPheSerGlyArgLeuArgAlaAspAsnThrLeuValLysSerCysArgGlu	524	; PRIOR FILING DATE: 2004-01-08			
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				; SOFTWARE: PatentIn version 3.3			
				; SEQ ID NO 3524			
				; LENGTH: 2947			
				; TYPE: DNA			
				; ORGANISM: Canis familiaris			
				PCT-US05-00517-3524			
				Alignment Scores:			
				Pred. No.:	7,79e-103	Length:	2947
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				Best Local Similarity:	46.02%	Mismatches:	210

Query Match: 47.69% Indels: 90
DB: 1 Gaps: 11
US-10-660-763-2 (1-752) x PCT-US05-00517-3524 (1-2947)
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DB 368 GACTGGGAATTACGGTTACTGTGAAACAGTGAAGAAATTTATGGCCCTCAGAGATAAAAGT 427
QY 41 AspArgGluTyrAlaGlyLeuLeuHisMetSerLeuGlnAspSerGlyGlnSer 60
DB 428 GATAAAGAATATGCATCTCTTACAGAACCTTTGTAATCAAGTTGATAAGGAAGTACT 487
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DB 548 GAACAACCTAGCAATCATGAAGACACATGCAGAGCCCTAAATTTCTGGACCCCTTACAC 607
QY 101 LysLeuSerLeuLeuIleArgGluGlnGlnLeuArgLysThrTyrSerGluGlnTrp 120
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QY 141 GlnTyrArgAlaLeuAlaArgAspSerAlaGlnAlaLysArgLysTyrGlnGluAla--- 159
DB 728 AGCTATAGACAGTTTAAATAAGAAATGAAATCTCTCCAAAGAGAAATATAAGAGCTTTA 787
QY 160 SerLysAspLysAspArgAspLysAlaLysAspLysTyrValArgSerLeuTrpLysLeu 179
DB 788 GCTAAAGGGGAAGAAACCGAAAGGCCAAGCAAGCATATGACAAAGCGCAATGAAACTT 847
QY 180 PheAlaHisAsnArgTyrValLeuGlyValArgAlaAlaGlnLeuHisGlnHis 199
DB 848 CATGTATTGCAATAATCATGATATGTCATGCAATGAAAGGGGCACAGCTTCATCAGAAATCAG 907
QY 200 HisHisGlnLeuLeuLeuProGlyLeuLeuArgSerLeuGlnAspLeuHisGluGluMet 219
DB 908 TATTATCACACCACACTTCCTTCTGCTTCTGACTCTCTTCAGAGATGCAAGAGAATG 967
QY 220 AlaCysIleLeuLysGluIleLeuGlnGluTyrLeuGluIleSerSerLeuValGlnAsp 239
DB 968 ATAAAGCACTAAAGGTATATTTGATGAATATACAGCCAGATACCACTCTCGTTACAGAG 1027
QY 240 GluValValAlaIleHisArgGluMetAlaAlaAlaAlaAlaArgIleGlnProGluAla 259
DB 1028 GAAATAGTGAATGTCCTAATAAGAGATTCAAATGTCAGTTGAAACAGATAGACCCCTCAGACA 1087
QY 260 GluTyrGlnGlyPheLeuArgGlnTyrGlySerAlaProAspValProProCysValThr 279
DB 1088 GAATATAATAATTTATAGATGTTTCAGAGAACACAGCGCTGCTAAAGAGCAAGAAATTTGAG 1147
QY 280 PheAspGluSerLeuLeuGluGluGlyGluProLeuGluProGlyGluLeuGlnLeuAsn 299
DB 1148 TTTGATACCTCTCTTACTAGAGAAATGAAATCTTCAGGCAAAATGAAATTTATGTGGAAT 1207
QY 300 GluLeuThrValGluSerValGlnHisThrLeuThrSerValThrAspGluLeuAlaVal 319
DB 1208 AATTTAAACAGCAGAAAGTTTGCAGATGATGTGAAAACTTTAGCAGAGCAATTTATACAG 1267
QY 320 AlaThrGluMetValPheArgArgGlnGluMetValThrGlnLeuGlnGlnLeuArg 339
DB 1268 ACACAGCAGATGCTTTGTAACAGAGAGGCTGCTCTGGAGCTAGAGAGAGAAATT--- 1324

QY 340 AsnGluGluGluAsnThrHisProArgGluArg-----ValGlnLeuLeuGly 355
DB 1325 -----GAGGAGTCTCTAAGACCTGTGAAAGAAAGTCTGATATTTGCTCTCTGCTAAGC 1378
QY 356 LysArgGlnValLeuGlnGluAlaLeuGlnGlnValAlaLeuCysSerGlnAla 375
DB 1379 CAAAACAGACACTAGAAAGAGCTGAAACACATGCTCAGCAGCTGAGATGCATCAGGCA 1438
QY 376 LysLeuGlnAlaGlnGlnGluLeuLeuGlnThrLysLeuGluHisLeuGlyProGlyGlu 395
DB 1439 AAGTTTACAGCACAGAAAGAAATTTACTAGACAAAGAAAGTACAAAGAAATGAAGGAAAGAG 1498
QY 396 ProProProValLeuLeuLeuGlnAspAspArgHisSerThrSerSerSerGluGlnGlu 415
DB 1499 CCACCTCCAGTAGTGAATTTATGAAGAGATGCACGATCAGTTACATCTATGGAAGAAAG 1558
QY 416 ArgGluGlyGlyArgThrProThrLeuGluIleLeuLysSerHisIleSerGlyIlePhe 435
DB 1559 GAG-----AGGCTATCCAAATTTGAGTCCATCCGTCATTCATTCATTCGTTGGAAATATT 1609
QY 436 Arg---ProLys-----PheSer----- 440
DB 1610 AGGTCTCAAAGTCTGCACCTGGCTCTTCAACATTTCTCTGATACGATCCCCATAAGTGAG 1669
QY 440 ----- 440
DB 1670 AAGCCCTTGGCAGAACAGGACTGTTACACCGTGCATTTCCAGAAATAGAACGCGCAAGAT 1729
QY 440 ----- 440
DB 1730 CTATTAAACACAGGAGACTTCTTGGTGGAGAGAGTCTATGGGAAACCTGGTGAATAT 1789
QY 441 -----Asn 441
DB 1790 GTCTTTCTCTATATTCTGATGACAAAGGAGACACTTTATCATACAATTTGTTGATAAT 1849
QY 442 LeuTyrArgLeuGluGlyGluGlyPheProSerIleProLeuLeuIleAspHisLeuLeu 461
DB 1850 CTATATCGATTGGAAGGCACCTGGTTTTTCAACATTTCTCAACATTTATAGATCATCACTAT 1909
QY 462 SerThrGlnGlnProLeuThrLysSerGlyValValLeuHisArgAlaValProLys 481
DB 1910 ACAACAAACAGGTCACTCACTAAGAGTCAGGTGAGTCTTCTGCTGAATCTCTATTCCTTAAG 1969
QY 482 Asp---LysTrpValLeuAsnHisGluAspLeuValLeuGlyGluGlnIleGlyArgGly 500
DB 1970 GATAAGAAATGGGTTCTCAATCAGAGAGATGCACATGGGAGAAATTTACTGGGCAAGGG 2029
QY 501 AsnPheGlyGluValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaValLys 520
DB 2030 AATTTTGGTGAAGTATATAGGGGCATATTAAAG---GATAAACCTGCTGTTGCTGTTAAA 2086
QY 521 SerCysArgGluThrLeuProAspLeuLysAlaLysPheLeuGlnGluAlaArgIle 540
DB 2087 ACATGTAAGAGAGATCTTCTCAGGAACCTGAAATAAAATTTTACAAAGGCGCAAAAT 2146
QY 541 LeuLysGlnTyrSerHisProAsnIleValArgLeuIleGlyValCysThrGlnLysGln 560
DB 2147 CTCAGCAATACCATCATCCCAATATTTGTCAAACTTATAGCGCTTTGCACACAAAGACAG 2206
QY 561 ProIleTyrIleValMetGluLeuValGlnGlyGlyAspPheLeuThrPheLeuArgThr 580
DB 2207 CCTATCTACATCATATTGGAACCTGGTTCCAGAGGATGATTTCTGCTCTTCTGAGAAAG 2266
QY 581 GluGlyAlaArgLeuArgValLysThrLeuLeuGlnMetValGlyAspAlaAlaAlaGly 600
DB 2267 AAGAAGATGAAATAAACTCAACCAATTAGTAGAGTTTTCATTAGATGCTGCTTCTGCT 2326
QY 601 MetGluTyrLeuGluSerLysCysIleHisArgAspLeuAlaAlaArgAsnCysLeu 620
DB 2327 ATGCTCTATCTCAGAGATAAATAACTGTATACACAGGATCTGGCTGCAAGNAACCTGCTG 2386
QY 621 ValThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAlaAsp 640

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2387 GTAGGTGAAAAATAACGTTCTGAAATCATGACATTGGAATGTCCTGCAAGAGGATGCT 2446
||||| ||| |||||||||||||||||||||||||||||||||||||||||||
641 GlyValTyrAlaAlaSerGlyGlyLeuArgGlnValProVallysTrpThrAlaProGlu 660
||||| |||||||||||||||||||||||||||||||||||||||||||
2447 GGAGTGATTTTCATCTTCT --GGCTTAAGCAGATTCCCATTAATGGACAGCACCAGAA 2503
||||| |||||||||||||||||||||||||||||||||||||||||||
661 AlaLeuAsnTyrGlyArgTyrSerSerGluSerAspValTyrSerPheGlyLeuLeu 680
||||| |||||||||||||||||||||||||||||||||||||||||||
2504 GCTCTTAATATGGGAGATACAGTTCTTGAGACGACGTGTGGAGCTTCGGCATCTCCCTC 2563
||||| |||||||||||||||||||||||||||||||||||||||||||
681 TrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnInThrArg 700
||||| |||||||||||||||||||||||||||||||||||||||||||
2564 TGGGAGACCTTCAGCTTAGAGTGTGCCCTACCCCGGAATGCACAAATCAGCAGCGCAGC 2623
||||| |||||||||||||||||||||||||||||||||||||||||||
701 GluPheValGluTysGlyArgLeuProCysProGluLeuCysProAspAlaValPhe 720
||||| |||||||||||||||||||||||||||||||||||||||||||
2624 GAGCAAGTGGAAAGAGGGTACCGAATATCAGCCCCCAGCATTCGCCAGAGACATTTT 2683
||||| |||||||||||||||||||||||||||||||||||||||||||
721 ArgLeuMetGluGlnCysTrpAlaTyrGluProGlyGlnArgProSerPheSerThrIle 740
||||| |||||||||||||||||||||||||||||||||||||||||||
2684 AAAATATATGATGCAAGTGTGGATTATAACCTGAAACCGCCCAAGTTCAGTGAACCT 2743
||||| |||||||||||||||||||||||||||||||||||||||||||
741 TyrGlnGluLeuGlnSerIleArgLysArg 750
||||| |||||||||||||||||||||||||||||||||||||||||||
2744 CAGAAAGAGCTCACGGTCATCAAGAGAAA 2773
||||| |||||||||||||||||||||||||||||||||||||||||||

RESULT 4
US-11-060-756-796
Sequence 796, Application US/11060756
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of
FILE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 796
LENGTH: 1400
TYPE: DNA
ORGANISM: Homo sapiens
US-11-060-756-796

Alignment Scores:
Pred. No.: 3,12e-91 Length: 1400
Score: 1654.00 Matches: 323
Percent Similarity: 82.19% Conservative: 0
Best Local Similarity: 82.19% Mismatches: 0
Query Match: 42.64% Indels: 70
DB: 19 Gaps: 1

US-10-660-763-2 (1-752) x US-11-060-756-796 (1-1400)
QY 430 HistLeSerGlyIlePheArgProLysPheSer----- 440
Db 1 CACATCTCAGGAAATCTCCGCCCAAGTTCCTGCTCCCTCCACCGCTCAGCTCATTCG 60
QY 440 ----- 440
Db 61 GAGGTGCAGAACCCCTGCATGAGCAGCTGTGTGTACATGGGGCCATCCGAGGGCAGAG 120
QY 440 ----- 440
Db 121 GTGGCTGAGCTGCTGTGTGCATCTCTGGGACTTCCTGGTGGGGAGAGCCAGGGCAGACG 180
QY 440 ----- 440
Db 181 GAGTACGTGCTGTGGTGTGTGGGATGGTCTGCCCGGACATTCATCATCAGTCTTGT 240

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QY
441 ---AsnLeuTyrArgLeuGluGlyGlyGlyPheProSerIleProLeuLeuIleAspHis 450

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; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5068
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-5068

Alignment Scores:
Pred. No.: 3.12e-91 Length: 1400
Score: 1654.00 Matches: 323
Percent Similarity: 82.19% Conservative: 0
Best Local Similarity: 82.19% Mismatches: 0
Query Match: 42.64% Indels: 70
DB: 19 Gaps: 1

US-10-660-763-2 (1-752) x US-11-060-756-5068 (1-1400)

Qy 430 HisIleSerGlyIlePheArgProLysPheSer----- 440
Db 1 CACATCTCAGGATCTTCCGCCCCAAGTTCTCGCTCCCTCCACCGCTGCAGCTCATTTCCG 60
Qy 440 ----- 440
Db 61 GAGGTGCAGAAAGCCCTGCATGACAGCTGTGTGTACCATGGGGCCATCCCGAGGGCAGAG 120
Qy 440 ----- 440
Db 121 GTGGCTGAGCTGTGGTGCACTCTGGGACCTTCCTGGTGGGAGAGACCAGGGCAAGCAG 180
Qy 440 ----- 440
Db 181 GAGTACGTGCTGCGTGCTGTGGGATGGTCTGCCCGCGCACTTCATCATCCAGTCTCTTG 240
Qy 441 ---AsnLeuTyArgLeuGluGlyGluGlyPheProSerIleProLeuLeuIleAspHis 459
Db 241 GATAACCTGTACCGACTGGGAAGGGGAAGGCTTCTAGCATCTTCTTGGCTCATCGACCAC 300
Qy 460 LeuLeuSerThrGlnGlnProLeuThrLysLysSerGlyValValLeuHisArgAlaVal 479
Db 301 CTACTGAGACCCAGCAGCCCTCCACCAAGAGAGTGTGTGTCTGCACAGGGCTGTG 360
Qy 480 ProLysPheTyTrpValLeuAsnHisGluAspLeuValLeuGlyGluGlnIleGlyArg 499
Db 361 CCCAAGGACAAGTGGGTGCTGAACCATGAGACCTGGTGTGGGTGAGCAGATTGGACGG 420
Qy 500 GlyAsnPheGlyGluValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaVal 519
Db 421 GGGAACTTTGGCGAAGTGTTCAGCGGACGCTCGAGCGCCGACACACCCCTGGTGGCGGTG 480
Qy 520 LysSerCysArgGluThrLeuProAspLeuLysAlaLysPheLeuGlnGluAlaArg 539
Db 481 AAGTCTTGTGAGAGAGCGTCTCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGG 540
Qy 540 IleLeuLysGlnTyTrpSerHisProAsnIleValArgLeuIleGlyValCysThrGlnLys 559
Db 541 ATCTGAAGCAGTACAGCCACCCCAACATCATGCGGTCTCATTTGGTGTCTGCGACCAAG 600
Qy 560 GlnProIleTyIleValMetGluLeuValGlnGlyAspPheLeuThrPheLeuArg 579
Db 601 CAGCCCATCTACATCGTCATGAGCTGTGCGAGGGGGCGAGCTTCCTGACCTTCCTCCCG 660
Qy 580 ThrGluGlyAlaArgLeuArgValLysThrLeuLeuGlnMetValGlyAspAlaAlaAla 599
Db 661 ACGAGAGGGGGCCCGCTCGGGGTGAGACTCTGCTGAGATGGTGGGGGATGAGCTGCT 720
Qy 600 GlyMetGluTyTrpLeuGluSerLysCysCysIleHisArgAspLeuAlaAlaArgAsnCys 619
Db 721 GGCAATGAGTACCTGGAGAGCAAGTGTGTCATCCACCGGACCTGGTGTCTGCGAACTGC 780
Qy 620 LeuValThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAla 639
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Db 781 CTGGTGACAGAGAAGATGCTCGAAGATCAGTGACTTTGGGATGTCCGAGAGGAAGCY 840
Qy 640 AspGlyValTyTrpAlaAlaSerGlyGlyLeuArgGlnValProValLysTrpThrAlaPro 659
|-----|
Db 841 GATGGGCTCTATGACGCTCAGGGGGCTCAGACCAAGTCCCGTGAAGTGGACCGCACCT 900
Qy 660 GluAlaLeuAsnTyArgTyTrpSerSerGluSerAspValTrpSerPheGlyIleLeu 679
|-----|
Db 901 GAGGCCCTTAACTACGCGCGCTACTCTCCGAAGCAGCGTGTGGAGCTTTGGCATCTTG 960
Qy 680 LeuTrpGluThrPheSerLeuGlyAlaSerProTyTrpProAsnLeuSerAsnGlnGlnThr 699
|-----|
Db 961 CTCTGGGAGACCTTCAGCTGGGGGCTCCCTCTATCCCACTCAGCAATCAGCAGACA 1020
Qy 700 ArgGluPheValGluLysGlyArgLeuProCysProGluLeuCysProAspAlaVal 719
|-----|
Db 1021 CGGGAGTTTGTGGAGAAGGGGGCGTCTGCCCTGCCAGAGCTGTGTCTGATGCGGTG 1080
Qy 720 PheArgLeuMetGluGlnCysTrpAlaTyGluProGlyGlnArgProSerPheSerThr 739
|-----|
Db 1081 TTCAGGCTCATGGAGCAGTGTCTGGGCTATGAGCTGGGAGCGGCCAGCTTCAGCAC 1140
Qy 740 IleTyGlnGluLeuGlnSerIleArgLysArgHisArg 752
|-----|
Db 1141 ATCTACGAGGCTGCAGACATCCGAAGCGGATCGG 1179

RESULT 6
US-11-097-143-18926
; Sequence 18926, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18926
; LENGTH: 3369
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-18926

Alignment Scores:
Pred. No.: 1.46e-63 Length: 3369
Score: 1206.50 Matches: 290
Percent Similarity: 52.52% Conservative: 138
Best Local Similarity: 35.58% Mismatches: 300
Query Match: 31.10% Indels: 87
DB: 22 Gaps: 14

US-10-660-763-2 (1-752) x US-11-097-143-18926 (1-3369)

Qy 1 MetGlyPheSerSerGluLeuCysSerProGlnGlyHisGlyValLeuGlnMetGln 20
|-----|
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Db 97 TTCAATACAAAGCAGTCATCACCAAGAGTCGGGGTCTGCTGTAATCCTATTCCA 156
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Qy 481 LysAsp---LysTrpValLeuAsnHisGluAspLeuValLeuGlyGluGlnIleGlyArg 499
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Db 157 AAGGATAAGAAATGGGTCTTCATATCATAGATGTTTCTATGGCAGAAATTCATGGGCAAG 216
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Qy 500 GlyAsnPheGlyGluValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaVal 519
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Db 217 GGGAAATTTGGTGAAGGTATACAGGGGCACACTGAAG---GATAAAACCCCTGTGTGTT 273
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Qy 520 LysSerCysArgGluThrLeuProAspLeuLysAlaLysPheLeuGlnGluAlaArg 539
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Db 274 AAAAGTGCAGGAGACCTGCTCAGGAACCTAAATAAGTTTACAGGAAGCAAA 333
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Qy 540 IleLeuLysGlnTrpSerHisProAsnIleValArgLeuIleGlyValCysThrGlnLys 559
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Db 334 ATTCTCAAGCAATATGATACCCCAATATTGTCAAACTTATAGCGGTGTCACACAAGA 393
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Qy 560 GlnProIleTyrIleValMetGluLeuValGlnGlyCysPheLeuThrPheLeuArg 579
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Db 394 CAGCCTGTCTACATATATGGAACCTGCTCCAGGAGGTGATTTCTGTCTTCTTGAGG 453
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Qy 580 ThrGluGlyAlaArgLeuArgValLysThrLeuLeuGlnMetValGlyAspAlaAla 599
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Db 454 AAGAGGAAGGACGAGCTAAAGTTGAACAGTGTGTGAGGTTTCTTGGAGCGTTGCTGCT 513
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Qy 600 GlyMetGluTyrLeuGluSerLysCysCysIleHisArgAspLeuAlaAlaArgAsnCys 619
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Db 514 GGCATGTGTATCTCGAGGGCAGAACTGCAATTCACAGGGACCTGGCTGCACGGAACTGC 573
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Qy 620 LeuValThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAla 639
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Db 574 CTGTGTAGTGAATAATATCTCTGAAATCAGTGACCTTTGGSAYGWSKCGGCAAGAGAC 633
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Qy 640 AspGlyValTyrAlaAlaSerGlyLeuArgGlnValProValLysTrpThrAlaPro 659
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Db 634 GGTGGAGTGATTTCATCTTCT---GGCTTAAAGCAGATTCCTCATTAARTGCACAGACCA 690
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Qy 660 GluAlaLeuAsnTyrGlyArgTyrSerSerGluSerAspValTrpSerPheGlyIleLeu 679
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Db 691 GAAGCACTGAATATGGAGAGATACAGCTCTGAAAGTACCGTGTGGAGCTTCGGCATCTG 750
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Qy 680 LeuTrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThr 699
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Db 751 CTCCTGGAGACCTTCAGCCTGGAGTCTGTCCTGACCTACCTGGGTGACAAACCAAGCA 810
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Qy 700 ArgGluPheValGluLysGlyArgLeuProCysProGluLeuCysProAspAlaVal 719
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Db 811 CGGGAACAAGTGGAGAGAGGTATCGGATGTACAGCCCCACAGAACTGTCCCGRGGAAAT 870
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Qy 720 PheArgLeuMetGluGlnCysTrpAlaTyrGluProGlyGlnArgProSerPheSerThr 739
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Db 871 TTTCACATCATGATGAAGTGTGGGATTCAGAACTGAAACCCCTGAAACCCCTTAAGTTCA 930
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Qy 740 IleTyrGlnGluLeuGlnSerIleArgLysArg 750
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Db 931 CTTCAAGAGAGCTCMCGCCCATCAAGAGAA 963
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
RESULT 9
US-11-060-756-3332
; Sequence 3332, Application US/11060756
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3332
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-060-756-3333
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; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-3332
Alignment Scores:
Pred. No.: 3,04e-55 Length: 600
Score: 1057.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.25% Indels: 0
DB: 19 Gaps: 0
US-10-660-763-2 (1-752) x US-11-060-756-3332 (1-600)
Qy 554 GlyValCysThrGlnLysGlnProIleTyrIleValMetGluLeuValGlnGlyArg 573
Db 1 GGTGTCTGCACCCAGAGCAGCCCATCTACATCTGTCATGGAGCTTGTGAGGGGGCGAC 60
Qy 574 PheLeuThrPheLeuArgThrGluGlyAlaArgLeuArgValLysThrLeuLeuGlnMet 593
Db 61 TTCTCTGACCTTCTCCGACGAGGGGGCCGCTGCGGTGAAGACTCTGCTGCAGATG 120
Qy 594 ValGlyAspAlaAlaAlaGlyMetGluTyrLeuGluSerLysCysCysIleHisArgAsp 613
Db 121 GTGGGGGATGTCAGCTGCTGGCATGGAGTACCTGGAGAGCAAGTGTGTCATCCCGGAC 180
Qy 614 LeuAlaAlaArgAsnCysLeuValThrGluLysAsnValLeuLysIleSerAspPheGly 633
Db 181 CTGGCTGTCTCGAAGTCCCTGCTGTGACAGAGAAGATGCTCTGAAGATCAGTGACTTTGG 240
Qy 634 MetSerArgGluGluAlaAspGlyValTyrAlaAlaSerGlyGlyLeuArgGlnValPro 653
Db 241 ATGTCCGAGAGAGAGCTGATGGGTCTATGAGGCTCAGGGGGCTCAGACAAAGTCCC 300
Qy 654 ValLysTrpThrAlaProGluAlaLeuAsnTyrGlyArgTyrSerSerGluSerAspVal 673
Db 301 GTGAAGTGGACCGACCTGAGGCCCTTAACTACGGCCGTACTCTCCGAAAGCGACGTG 360
Qy 674 TrpSerPheGlyIleLeuLeuTrpGluThrPheSerLeuGlyAlaSerProTyrProAsn 693
Db 361 TGGAGCTTTGGCATCTTCTCTGGAGAGCTTTCAGCCTGGGGGCTTCCCTATCCCAAC 420
Qy 694 LeuSerAsnGlnGlnThrArgGluPheValGluLysGlyArgLeuProCysProGlu 713
Db 421 CTCAAGCAATCAGCAGACACGGAGTTTGTGGAGAGGGGGCGCTCTGCCCTGCCAGAG 480
Qy 714 LeuCysProAspAlaValPheArgLeuMetGluGlnCysTrpAlaTyrGluProGlyGln 733
Db 481 CTGTGTCTGTATGCCGTGTTCAGGCTCATGGAGCAGTGTGGGCTTATGAGCTTGGCAG 540
Qy 734 ArgProSerPheSerThrIleTyrGlnGluLeuGlnSerIleArgLysArgHisArg 752
Db 541 CGGCCCGAGCTTCAGCAGCACTTACCAGGAGTGCAGAGCATCCGAAAGCGGATCGG 597
RESULT 10
US-11-060-756-3333
; Sequence 3333, Application US/11060756
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3333
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-060-756-3333
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Alignment Scores:

Pred. No.: 3,04e-55 Length: 600
Score: 1057.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.25% Indels: 0
DB: 19 Gaps: 0

US-10-660-763-2 (1-752) x US-11-060-756-3333 (1-600)

Qy 554 GlyValCysThrGlnLysGlnProIleTyrlleValMetGluLeuValGlnGlyAsp 573
Db 1 GGTGTCTGCACCCAGAGCAGCCCATCTACATCGTCATGGAGCTTGTGACGGGGGGGAC 60
Qy 574 PheLeuThrPheLeuArgThrGluGlyAlaArgLeuArgValLysThrLeuLeuGlnMet 593
Db 61 TTCCTGACCTTCTCCGACGAGGGGGCGCTCGGGGTGAAGACTCTGCTGCAGATG 120
Qy 594 ValGlyAspAlaAlaGlyMetGluTyrlleValMetGluLysCysCysIleHisArgAsp 613
Db 121 GTGGGGATGTCAGTCTGCGACGAGGGGGCGCTCGGGGTGAAGACTCTGCTGCAGATG 180
Qy 614 LeuAlaAlaArgAsnCysLeuValThrGluLysAsnValLeuLysIleSerAspPheGly 633
Db 181 CTGGCTCTCGAACTCGCTGTCGATGAGTACCTGAGAGCAAGTCTGCTGCATCCACCGGGAC 180
Qy 634 MetSerArgGluGluAlaAspGlyValTyrlleValMetGluLysCysCysIleHisArgAsp 653
Db 241 ATGTCCTGCTCGAACTCGCTGTCGATGAGTACCTGAGAGCAAGTCTGCTGCATCCACCGGGAC 240
Qy 654 ValLysTrpThrAlaProGluAlaAspGlyValTyrlleValMetGluLysCysCysIleHisArgAsp 673
Db 301 GTGAAGTGGACCGCACCTTAACTACCGCGCGCTACTCTCCGAAAGCGAGTG 360
Qy 674 TrpSerPheGlyIleLeuLeuTrpGluThrPheSerLeuGlyAlaSerProTyrlleProAsn 693
Db 361 TGGAGCTTTGGCATCTTGTCTCTGGAGACCTTACGCGCGCTACTCTCCGAAAGCGAGTG 360
Qy 694 LeuSerAsnGlnGlnThrArgGluPheValGluLysGlyArgLeuProCysProGlu 713
Db 421 CTCAGCAATCAGCAGACACGGAGTTTGTGAGAGGGGGCGCTCTGCGCTGCGCCAGAG 480
Qy 714 LeuCysProAspAlaValPheArgLeuMetGluGlnCysTrpAlaTyrlleGluProGlyGln 733
Db 481 CTGTGCTCTGATCGCGTTTCAGGCTCATGAGCAGTCTGCGCTATGAGCCTTGGGCGAG 540
Qy 734 ArgProSerPheSerThrIleTyrlleGluLeuGlnSerIleArgLysArgHisArg 752
Db 541 CGGCCAGCTTCAGCACCATCTACAGAGCTGTCAGAGCATCCGAAAGCGGCATCGG 597

RESULT 11

US-11-060-756-7604
; Sequence 7604, Application US/11060756
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7604
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-7604

Alignment Scores:
Pred. No.: 3,04e-55 Length: 600
Score: 1057.00 Matches: 199

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.25% Indels: 0
DB: 19 Gaps: 0

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.25% Indels: 0
DB: 19 Gaps: 0

US-10-660-763-2 (1-752) x US-11-060-756-7604 (1-600)

Qy 554 GlyValCysThrGlnLysGlnProIleTyrlleValMetGluLeuValGlnGlyAsp 573
Db 1 GGTGTCTGCACCCAGAGCAGCCCATCTACATCGTCATGGAGCTTGTGACGGGGGGGAC 60
Qy 574 PheLeuThrPheLeuArgThrGluGlyAlaArgLeuArgValLysThrLeuLeuGlnMet 593
Db 61 TTCCTGACCTTCTCCGACGAGGGGGCGCTCGGGGTGAAGACTCTGCTGCAGATG 120
Qy 594 ValGlyAspAlaAlaGlyMetGluTyrlleValMetGluLysCysCysIleHisArgAsp 613
Db 121 GTGGGGATGTCAGTCTGCGACGAGGGGGCGCTCGGGGTGAAGACTCTGCTGCAGATG 180
Qy 614 LeuAlaAlaArgAsnCysLeuValThrGluLysAsnValLeuLysIleSerAspPheGly 633
Db 181 CTGGCTCTCGAACTCGCTGTCGATGAGTACCTGAGAGCAAGTCTGCTGCATCCACCGGGAC 240
Qy 634 MetSerArgGluGluAlaAspGlyValTyrlleValMetGluLysCysCysIleHisArgAsp 653
Db 241 ATGTCCTGCTCGAACTCGCTGTCGATGAGTACCTGAGAGCAAGTCTGCTGCATCCACCGGGAC 300
Qy 654 ValLysTrpThrAlaProGluAlaAspGlyValTyrlleValMetGluLysCysCysIleHisArgAsp 673
Db 301 GTGAAGTGGACCGCACCTTAACTACCGCGCGCTACTCTCCGAAAGCGAGTG 360
Qy 674 TrpSerPheGlyIleLeuLeuTrpGluThrPheSerLeuGlyAlaSerProTyrlleProAsn 693
Db 361 TGGAGCTTTGGCATCTTGTCTCTGGAGACCTTACGCGCGCTACTCTCCGAAAGCGAGTG 420
Qy 694 LeuSerAsnGlnGlnThrArgGluPheValGluLysGlyArgLeuProCysProGlu 713
Db 421 CTCAGCAATCAGCAGACACGGAGTTTGTGAGAGGGGGCGCTCTGCGCTGCGCCAGAG 480
Qy 714 LeuCysProAspAlaValPheArgLeuMetGluGlnCysTrpAlaTyrlleGluProGlyGln 733
Db 481 CTGTGCTCTGATCGCGTTTCAGGCTCATGAGCAGTCTGCGCTATGAGCCTTGGGCGAG 540
Qy 734 ArgProSerPheSerThrIleTyrlleGluLeuGlnSerIleArgLysArgHisArg 752
Db 541 CGGCCAGCTTCAGCACCATCTACAGAGCTGTCAGAGCATCCGAAAGCGGCATCGG 597

RESULT 12

US-11-060-756-7605
; Sequence 7605, Application US/11060756
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7605
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-7605

Alignment Scores:
Pred. No.: 3,04e-55 Length: 600
Score: 1057.00 Matches: 199
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 27.25% Indels: 0
DB: 19 Gaps: 0

```
US-10-660-763-2 (1-752) x US-111-060-756-7605 (1-600)
QY 554 GilyValCysThrGlnLysGlnProIleTyrIleValMetGluLeuValGlnGlyGlyAsp 573
Db 1 GGTGTCTGCACCCAGAGCAGCCCATCTACATCGTCATGAGCTTGTGCAGGGGGCGAC 60
QY 574 PheLeuThrPheLeuArgThrGluGlyAlaArgLeuArgValLysThrLeuLeuGlnMet 593
Db 61 TTCTGACCTTCTCCGCACGAGAGGGGGCCGCTGCGGGTGAAGACTCTGCTGCAGATG 120
QY 594 ValGlyAspAlaAlaGlyMetGluTyrLeuGluSerLysCysCysIleHisArgAsp 613
Db 121 GTGGGGATGCAGCTGCTGCATGGAGTACTCTGGAGAGCAAGTGTCTCATCCACCGGAC 180
QY 614 LeuAlaAlaArgAenCysLeuValThrGluLysAenValLeuLysIleSerAspPheGly 633
Db 181 CTGGCTCTCGGAAGTCTGCTGGTGCACAGAGAAATGCTCCTGAGATCATGAGCTTTGGG 240
QY 634 MetSerArgGluGluAlaAspGlyValTyrAlaAlaSerGlyGlyLeuArgGlnValPro 653
Db 241 ATGTCCCGAGAGGAGCTGATGGGGTCTATGCAGCCTCAGGGGGCTCAGACAAAGTCCCC 300
QY 654 ValLysTrpThrAlaProGluAlaLeuAenTyrGlyArgTyrSerSerGluSerAspVal 673
Db 301 GTGAAGTGGACCGCACCTGAGGGCCCTTAACCTACGGCCGCTACTCTCCGAAAGCGAGTG 360
QY 674 TrpSerPheGlyIleLeuLeuTrpGluThrPheSerLeuGlyAlaSerProTyrProAen 693
Db 361 TGGAGCTTTGGCATCTTGTCTCTGGAGACCTTACGCTGGGGGCTCCCTCATTCCTCAAC 420
QY 694 LeuSerAenGlnGlnThrArgGluPheValGluLysGlyArgLeuProCysProGlu 713
Db 421 CTAGCAATCAGCAGACACGGGAGTTTGTGGAGAGGGGGCGCTGTGCCCTGCCAGAG 480
QY 714 LeuCysProAspAlaValPheArgLeuMetGluGlnCysTrpAlaTyrGluProGlyGln 733
Db 481 CTGTGCTCTGATCGCGTTCAGGCTCATGAGCAGTGTCTGGGCTATGAGCCTGGGCAG 540
QY 734 ArgProSerPheSerThrIleTyrGlnGluLeuGlnSerIleArgLysArgHisArg 752
Db 541 CGGCCCCAGCTTCAGCACCATCTACAGAGCTGAGAGCATCCGAAAGCGGCATCGG 597

RESULT 13
US-60-680-544-39317
; Sequence 39317, Application US/60680544
; GENERAL INFORMATION:
; APPLICANT: Cooper, Matthew
; APPLICANT: Kinch, Deborah
; APPLICANT: Rosenberg, Michael
; APPLICANT: Subramaniam, S. Sai
; APPLICANT: Szak, Suzanne
; APPLICANT: Li, Huo
; APPLICANT: Bandaru, Raj
; APPLICANT: Derbel, Maher
; TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary
; FILE REFERENCE: 21590290000
; CURRENT APPLICATION NUMBER: US/60/680,544
; NUMBER OF SEQ ID NOS: 48714
; SOFTWARE: Patent Sequence Analysis Tool Version 1.0
; SEQ ID NO 39317
; LENGTH: 638
; TYPE: DNA
; ORGANISM: Macaca Mulatta
US-60-680-544-39317
Alignment Scores: 8.88e-53 Length: 638
Pred. No.: 1017.00 Matches: 196
Score: 99.50%
Percent Similarity: 99.50%
Best Local Similarity: 98.00% Mismatches: 3
Mismatches: 1
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Query Match: 26.22% Indels: 0
DB: 23 Gaps: 0
US-10-660-763-2 (1-752) x US-60-680-544-39317 (1-638)
QY 1 MetGlyPheSerSerGluLeuCysSerProGlnGlyHisGlyValLeuGlnMetGln 20
Db 39 ATGGGCTTCTCTTCGAGAGTGTGCACCCCGGCGCACCGGGTCTCTGCAGCAGATGCGAG 98
QY 21 GluAlaGluLeuArgLeuGluGlyMetArgLysTrpMetAlaGlnArgValLysSer 40
Db 99 GAGGCTGAGCTTCTGTCTACTGAGGGCATGAGAAAGTGGATGGCCCAACGGGTCAAGAGT 158
QY 41 AspArgGluTyrAlaGlyLeuLeuHisMetSerLeuGlnAspSerGlyGlyGlnSer 60
Db 159 GACAGGGAGTATGACGAGTGTCTTACCACATGTCCGTGCAGACAGTGGGGGCCAGAGC 218
QY 61 ArgAlaIleSerProAspSerProIleSerGlnSerTrpAlaGluIleThrSerGlnThr 80
Db 219 CGGGGCATCAGCCCTGACAGCCCATCAGCAGTCTCTGGCGGAGATCTGAACCTCAGGGCCCAACT 278
QY 81 GluGlyLeuSerArgLeuLeuArgGlnHisAlaGluAspLeuAenSerGlyProLeuSer 100
Db 279 GAGGGCCTCAGCGGTTGCTGGCGCAGCACCGGAGGATCTGAACCTCAGGGCCCTTGAGC 338
QY 101 LysLeuSerLeuLeuIleArgGluArgGlnGlnLeuArgLysThrTyrSerGluGlnTrp 120
Db 339 AGTTGAGCTGCTCATCCGGGACCGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTGG 398
QY 121 GlnGlnLeuGlnGlnLeuThrLysThrHisSerGlnAspIleGluLysLeuLysSer 140
Db 399 CAGCAGCTCAGCAGGAGCTCCACCAAGACTCAGCAGCAGGACATTTGAGAAGCTTGAAGAGC 458
QY 141 GlnTyrArgAlaLeuAlaArgAspSerAlaGlnAlaLysArgLysTyrGlnGluAlaSer 160
Db 459 CAGTACCGAGCCCTTGCCACCGGACAGTGCCTCCCAAGCCCAAGCAGTACCGAGGGCCAGC 518
QY 161 LysAspLysAspArgAspLysAlaLysAspLysTyrValArgSerLeuTrpLysLeuPhe 180
Db 519 AAAGCAAGGACCGCTGACAAAGCCAAAGGACAAAGTATGTGGCAGCCTGTGGAAGCTCTTT 578
QY 181 AlaHisHisAenArgTyrValLeuGlyValArgAlaAlaGlnLeuHisGlnHis 200
Db 579 GCTCACCAACCGCTATGTCTGGGCGTGTGGGCTGCAGCTACACTACCAGCACCAC 638

RESULT 14
US-60-680-473-39317
; Sequence 39317, Application US/60680473
; GENERAL INFORMATION:
; APPLICANT: Cooper, Matthew
; APPLICANT: Kinch, Deborah
; APPLICANT: Rosenberg, Michael
; APPLICANT: Subramaniam, S. Sai
; APPLICANT: Szak, Suzanne
; APPLICANT: Li, Huo
; APPLICANT: Bandaru, Raj
; APPLICANT: Derbel, Maher
; TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary
; FILE REFERENCE: 21590290000
; CURRENT APPLICATION NUMBER: US/60/680,473
; NUMBER OF SEQ ID NOS: 48714
; SOFTWARE: Patent Sequence Analysis Tool Version 1.0
; SEQ ID NO 39317
; LENGTH: 638
; TYPE: DNA
; ORGANISM: Macaca Mulatta
US-60-680-473-39317
Alignment Scores: 8.88e-53 Length: 638
Pred. No.: 1017.00 Matches: 196
Score: 99.50% Mismatches: 1
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Percent Similarity: 99.50% Conservative: 3
Best Local Similarity: 98.00% Mismatches: 1
Query Match: 26.22% Indels: 0
DB: 23 Gaps: 0

US-10-660-763-2 (1-752) x US-60-680-473-39317 (1-638)

Qy 1 MetGlyPheSerSerGluLeuCySerProGlnGlyHisGlyValLeuGlnGlnMetGln 20
Db 39 ATGGGCTTCTCTCGAGCTGTGACCCGCCCGCCCGGCTCTCGAGCAGATGCG 98

Qy 21 GluAlaGluLeuArgLeuGluGlyMetArgLysTrpMetAlaGlnArgValLysSer 40
Db 99 GAGGCTGAGCTTCTCTCGAGGATGAGAAGTGGATGGCCCAACGGGTCAAGAGT 158

Qy 41 AspArgGluTyrAlaGlyLeuLeuHisMetSerLeuGlnAspSerGlyGlyGlnSer 60
Db 159 GACAGGAGATGTCAGAGCTCTTCCACCATGTCCTGTCAGGACAGTGGGGCCAGC 218

Qy 61 ArgAlaLeuSerProAspSerProIleSerGlnSerTrpAlaGluLeuThrSerGlnThr 80
Db 219 CGGGGCTATGAGCTGACAGCCCATCAGCCAGTCTTGGCGGAGATCACCAGCCAACT 278

Qy 81 GluGlyLeuSerArgLeuLeuArgGlnHisAlaGluAspLeuAsnSerGlyProLeuSer 100
Db 279 GAGGGCTGAGCCGGTGTCTGCGGACGACCGGAGGATCTGAACCTCAGGCGCCCTGAGC 338

Qy 101 LysLeuSerLeuLeuLeuArgGluArgGlnGlnLeuArgLysTrpTyrSerGluGlnTrp 120
Db 339 AAGTTGAGCTTCTATCCGGGAACGCGAGCAGCTTGCAGACCTCAGGACAGCTGG 398

Qy 121 GlnGlnLeuGlnGlnLeuThrLysThrHisSerGlnAspIleGluLysLeuLysSer 140
Db 399 CAGCAGCTGACAGGAGCTCACCAGACTCACAGCCAGGACATTGAGAAGCTGAAGAGC 458

Qy 141 GlnTyrArgAlaLeuAlaArgAspSerAlaGlnAlaLysArgLysTrpGlnGlnLysSer 160
Db 459 CAGTACCGAGCCCTGGCAGCGGACAGTCCCAAGCCAAAGCGCAAGTACCAGGCGCAGC 518

Qy 161 LysAspLysAspArgAspLysAlaLysAspLysTrpValArgSerLeuTrpLysPhe 180
Db 519 AAGACAAAGGACCTGTGACAGCCAGGACCAAGTATGTGCCAGCTCTGTGAAGCTCTTT 578

Qy 181 AlaHisHisAsnArgTyrValLeuGlyValArgAlaAlaGlnLeuHisGlnHis 200
Db 579 GCTCACCAACCCGTATGTCTGGCGTGGCGCTGCGGCTGCACAGCTACACTACCAGCCAC 638

RESULT 15

US-11-097-143-24845
; Sequence 24845, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24845
; LENGTH: 3198
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-24845

Alignment Scores:
Pred. No.: 8 5e-52 Length: 3198
Score: 1013.00 Matches: 257
Percent Similarity: 42.44% Conservative: 108
Best Local Similarity: 29.88% Mismatches: 245
Query Match: 26.11% Indels: 250
DB: 22 Gaps: 13

US-10-660-763-2 (1-752) x US-11-097-143-24845 (1-3198)

Qy 122 GlnLeuGlnGlnGlnLeuThrLysThrHisSerGlnAspIleGluLysLeuLysSerGln 141
Db 1 CAGCTCACCCAGCAGGTGGTGGCAAGAAATCT--GAATACCAAAACATTTGGAGGCG 57

Qy 142 TyrArgAlaLeuAlaArgAspSerAlaGlnAlaLysArgLysTrpGlnGlnAlaSerLys 161
Db 58 TACAAGCGCTG-----CGCAGCGCTTCGAGGAGAACTACATAAAGGACCCAGT 108

Qy 162 AspLysAspArg-----AspLysAlaLysAspLysTrpValArgSerLeuTrpLysLeu 179
Db 109 CGCAGTGGCGCGAAGCTGGACGATGCGTGACAAAGTATCAGAAAGGCTTCGCCCAATTG 168

Qy 180 PheAlaHisHisAsnArgTyrValLeuGlyValArgAlaAlaGlnLeuHisGlnHis 199
Db 169 CATCTCACACACACGAGTACGTGCTCATCAGCGAAGCCATCGAAGTGGAGAGGAC 228

Qy 200 HisHisGlnLeuLeuProGlyLeuLeuArgSerLeuGlnAspLeuHisGluGluMet 219
Db 229 TTTCCGCAACCTTGTGTCGGGACTGCTGAGCATCAGCAGCTCCGTTTCAGGAGAGTTC 288

Qy 220 AlaCysIleLeuLysGluIleLeuGlnGluTyrLeuGluLysSerSerLeuValGluAsp 239
Db 289 ATCTGCTGTGGCGCAACATCTGCGAGGAGCGCGCCCGATGTCGCGACCTCAGCGCGAC 348

Qy 240 GluValValAlaIleHisArgGluMetAlaAlaAlaAlaArgIleGlnProGluAla 259
Db 349 AAGTACAAGGAGATCCAGAAGCGCATTTGACACTGTGATAGGAGCATCAATCCGACCGAG 408

Qy 260 GluTyrGlnGlyPheLeuArgGlnTyrGlySerAlaProAspValProProCysValThr 279
Db 409 GAGTACGGCGAGTTTCCCGAGAAATACAAAACCTCTCCCAACACCGCTGCTCTCCAG 468

Qy 280 PheAspGluSerLeuLeuGluGlyGluProLeuGluProGlyGluLeuGlnLeuAsn 299
Db 469 TTCGATGAGACGCTCATCCAGGAT-----ATTCGCGCAAAATTCGATCGCAGC 516

Qy 300 GluLeuThrValGluSerValGlnHisThrLeuThrSerValThrAspGluLeuAlaVal 319
Db 517 ACATTGACATGGACAACTC-----ACGGTGGAGTGGCTGCTGCTATCTCCAGAA 570

Qy 320 AlaThrGluMetValPheArgArgGlnGluMetValThrGlnLeuGlnGlnLeuArg 339
Db 571 CTGGAGGAGCGCTCAGGGATTGCCAGGAGAAG-----CAGATGAAGATGATC 618

Qy 340 AsnGluGluGlnAsnThrHisProArgGluArgValGlnLeuLeuGlyLysArgGlnVal 359
Db 619 GAGCATGTGAATGGTGGCTCGCCGGTGGCCAAATGGCAGCATTATATCCACGCGCAGAAC 678

Qy 360 LeuGlnGlnAlaLeuGlnGlyLeuGlnValAlaLeuCysSerGlnAlaLys----- 376
Db 679 ACATCCAAACGGCAATTCAGTCCAAACAGGATAGCTATGTCGCCCGCCAGGACCTTAAT 738

Qy 377 ---LeuGlnAlaGlnGln-----GluLeuLeuGlnThrLysLeu 388

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 10, 2005, 09:00:04 ; Search time 1599 Seconds
(without alignments)
3048.598 Million cell updates/sec

Title: US-10-660-763-2

Perfect score: 3879

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Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA -QFMT=fastp -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62
-TRANS=human40.cdi -LIST=45 -DCAALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:
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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3879	100.0	2674	13 US-10-003-295-1	Sequence 1, Appli
2	3879	100.0	2674	18 US-10-660-763-1	Sequence 1, Appli
3	3821	98.5	2889	16 US-10-240-965-256	Sequence 256, App
4	2137	55.1	15297	13 US-10-003-295-3	Sequence 3, Appli
5	2137	55.1	15297	18 US-10-660-763-3	Sequence 3, Appli
6	1853	47.8	2950	21 US-10-887-553A-240	Sequence 240, App
7	892	23.0	1779	18 US-10-280-576-19	Sequence 19, Appl
8	624.5	16.1	449	10 US-09-918-995-1503	Sequence 1503, Ap
9	624.5	16.1	3840	16 US-10-204-041-3	Sequence 3, Appli
10	624.5	16.1	3840	19 US-10-717-597-234	Sequence 234, App
11	624.5	16.1	3840	19 US-10-802-432-26	Sequence 26, Appl
12	624.5	16.1	5434	17 US-10-170-385-182	Sequence 182, App
13	624.5	16.1	5744	17 US-10-439-703-5	Sequence 5, Appli
14	623	16.1	3450	17 US-10-457-954-5	Sequence 5, Appli
15	622	16.0	3393	16 US-10-263-480-1	Sequence 1, Appli
16	622	16.0	5527	9 US-09-880-107-3710	Sequence 3710, Ap
17	620.5	16.0	3653	17 US-10-258-666-7	Sequence 7, Appli
18	620.5	16.0	4705	16 US-10-312-918-1	Sequence 1, Appli
19	620.5	16.0	4786	16 US-10-312-918-3	Sequence 3, Appli
20	608	15.7	1518	18 US-10-280-576-24	Sequence 24, Appl
21	607.5	15.7	1713	9 US-09-741-154-1	Sequence 1, Appli
22	607.5	15.7	1713	16 US-10-187-900-1	Sequence 1, Appli
23	605.5	15.6	1933	21 US-10-895-225A-10	Sequence 10, Appl
24	605.5	15.6	2000	9 US-09-977-260-1	Sequence 1, Appli
25	605.5	15.6	2000	10 US-09-977-261-1	Sequence 1, Appli
26	605.5	15.6	2104	21 US-10-895-225A-9	Sequence 9, Appli
27	605.5	15.6	2193	21 US-10-895-225A-11	Sequence 11, Appl
28	603.5	15.6	3645	18 US-10-280-576-10	Sequence 10, Appl
29	598	15.4	1995	16 US-10-378-393-6	Sequence 6, Appli
30	598	15.4	2574	9 US-09-735-103-2	Sequence 2, Appli
31	598	15.4	2574	13 US-10-045-428A-2	Sequence 2, Appli
32	598	15.4	2604	15 US-10-171-581-317	Sequence 317, App
33	598	15.4	2604	17 US-10-353-690-33	Sequence 33, Appl
34	598	15.4	8858	16 US-10-378-393-1	Sequence 1, Appli
35	597	15.4	3650	17 US-10-369-022-59	Sequence 59, Appl
36	597	15.4	3650	17 US-10-366-288-17	Sequence 17, Appl
37	597	15.4	3650	21 US-10-497-692-1	Sequence 1, Appli
38	596.5	15.4	3663	9 US-09-919-172-84	Sequence 84, Appl
39	596.5	15.4	3663	20 US-10-752-985-84	Sequence 84, Appl
40	592.5	15.3	3593	15 US-10-220-801-6	Sequence 6, Appli
41	591	15.2	2449	15 US-10-220-801-11	Sequence 11, Appl
42	591	15.2	2456	13 US-10-186-399-1	Sequence 1, Appli
43	591	15.2	2456	16 US-10-021-660-41	Sequence 41, Appl
44	591	15.2	2456	17 US-10-305-720-1476	Sequence 1476, Ap
45	591	15.2	2456	18 US-10-211-462-128	Sequence 128, App

ALIGNMENTS

RESULT 1

US-10-003-295-1
; Sequence 1, Application US/10003295
; Publication No. US20020168741A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THERSOF
; FILE REFERENCE: CLO01183DIV
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2674

TYPE: DNA
ORGANISM: Homo sapiens
US-10-003-295-1

Alignment Scores:

Pred. No.: 0 Length: 2674
Score: 3879.00 Matches: 752
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-660-763-2 (1-752) x US-10-003-295-1 (1-2674)

QY 1 MetGlyPheSerSerGluLeuLeuCysSerProGlnGlyHisGlyValLeuGlnMetGln 20
DB 72 ATGGGCTTCTCTTCTGAGCTGTGCAGCCCGCCAGGGCCACGGGGTCTCGAGCAAAATGCGAG 131
QY 21 GluAlaGluLeuArgLeuLeuGluGlyMetArgLysTrpMetAlaGlnArgValLysSer 40
DB 132 GAGCCGAGCTTCTCTACTGGAGGGCATGAGAAAGTGGATGGCCCGAGCGGTCAAGAGT 191
QY 41 AspArgGluTyrAlaGlyLeuLeuHisHisMetSerLeuGlnAspSerGlyGlnSer 60
DB 192 GACAGGGAGTATGACGAGCTGCTTACCACATGTCTGCGAGACAGTGGGGGCCAGAGC 251
QY 61 ArgAlaIleSerProAspSerProIleSerGlnSerTrpAlaGluIleThrSerGlnThr 80
DB 252 CGGGCCATCATCGCCCTGACAGCCCATCAGTCAGTCCTGGGCTGAGATCACCGCCAAACT 311
QY 81 GluGlyLeuSerArgLeuLeuArgGlnHisAlaGluAspLeuAsnSerGlyProLeuSer 100
DB 312 GAGGGCTGAGCGCTGTCTGCGGAGCAGCAGAGGATCTGAACCTCAGGGCCCTTGAGC 371
QY 101 LysLeuSerLeuLeuLeuArgGluArgGlnGlnLeuArgLysThrTyrSerGluGlnTrp 120
DB 372 AAGCTGAGCCTGTCTATCCGGGAACCGCAGCAGCTTCGCAAGACCTACACGCGAGCAGTGG 431
QY 121 GlnGlnLeuGlnGlnLeuThrLysThrHisSerGlnAspIleGluLysLeuLysSer 140
DB 432 CAGCAGCTGACGAGGAGCTCACCAAGACCACAGCCAGCAGACATTTGAGAAGCTGAAGAGC 491
QY 141 GlnTyrArgAlaLeuAlaArgAspSerAlaGlnAlaLysArgLysTyrGlnGluAlaSer 160
DB 492 CAGTACCGAGCTCTGGCACCGGACAGTCCCAAGCCAAAGCGCAAGTACAGAGGCGCAGC 551
QY 161 LysAspLysAspArgAspLysAlaLysAspLysTyrValArgSerLeuTrpLysLeuPhe 180
DB 552 AAAGACAAGGACCGTGAACAAGGCCAAGGACAAGTATGTGGCGAGCCTGTGGAAAGCTCTTT 611
QY 181 AlaHisHisAsnArgTyrValLeuGlyValArgAlaAlaGlnLeuHisHisGlnHis 200
DB 612 GCTCACCAACCGCTATGTCTGGGGCTGGGGCTGGCGAGCTACACCAACGAGCACCCAC 671
QY 201 HisGlnLeuLeuLeuProGlyLeuLeuArgSerLeuGlnAspLeuHisGluGluMetAla 220
DB 672 CACCAGCTCTGCTGTCGCGGCTGCTGCGGTCTACTGCGAGACCTGCGACGAGGAGATGGCT 731
QY 221 CysIleLeuLysGluIleLeuGlnGlnLysLeuGluIleSerSerLeuValGlnAspGlu 240
DB 732 TGCATCTGGAAGGAGATCTCTGCAAGGAATACCTGAGATTAGCAGCCCTGGTGGAGGATGAG 791
QY 241 ValValAlaIleHisArgGluMetAlaAlaAlaAlaArgIleGlnProGluAlaGlu 260
DB 792 GTGGTGGCCATTACCGGGAGATGGCTGCGAGCTGCTGCCCGCATCCAGCCTGAGGCTGAG 851
QY 261 TyrGlnGlyPheLeuArgGlnTyrGlySerAlaProAspValProProCysValThrPhe 280
DB 852 TACCAAGGCTTCTCGCACAGTATGGGTCCGCACCTGACGTCCACCCCTGTGTCAAGTTC 911
QY 281 AspGlnSerLeuLeuGluGlyGluProLeuGluProGlyGluLeuGlnLeuAsnGlu 300
DB 912 GATGAGTCACTGCTTGAGGAGGGTGAACCCGCTGGAGCTGGGAGCTCCAGCTGAACGAG 971

QY 301 LeuThrValGluSerValGlnHisThrLeuThrSerValThrAspGluLeuAlaValAla 320
DB 972 CTGACTGTGGAGAGCGTGCAGCACACCGTGCCTCAGTGCAGATGAGCTGGCTGTGGCC 1031
QY 321 ThrGluMetValPheArgGlnGluMetValThrGlnLeuGlnGlnLeuArgAsn 340
DB 1032 ACCGAGATGGTGTTCAGGGCGGCGAGAGATGGTTACGACAGTGCACACAGAGCTCCGGAAT 1091
QY 341 GluGluGluAsnThrHisProArgGluArgValGlnLeuLeuGlyLysArgGlnValLeu 360
DB 1092 GAAAGAGAGAACACACCCCGCGGAGCGGTGTCAGCTGCTGGGCAAGAGGCAAGTGCTG 1151
QY 361 GlnGluAlaLeuGlnGlnLeuGlnValAlaLeuCysSerGlnAlaLysLeuGlnAlaGln 380
DB 1152 CAAAGAACCATGTCAGGGGCTGCAGGTAGCGCTGTGCAGCCAGGCCCAAGCTGCAGGCCAG 1211
QY 381 GlnGluLeuLeuGlnThrLysLeuGluHisLeuGlyProGlyGluProProValLeu 400
DB 1212 CAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGCCCGCGGAGCCCCCGCTGTGCTG 1271
QY 401 LeuLeuGlnAspAspArgHisSerThrSerSerSerGluGlnGluArgGluGlyArg 420
DB 1272 CTCCTGCAGGATGACCGCCACTCCACGTGCTCCTCGGAGCAGGAGCGAGGGGGAGG 1331
QY 421 ThrProThrLeuGluIleLeuLysSerHisIleSerGlyIlePheArgProLysPheSer 440
DB 1332 ACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCGCGCCCAAGTCTCG 1391
QY 441 AsnLeuTyrArgLeuGluGlyGluGlyPheProSerIleProLeuLeuIleAspHisLeu 460
DB 1392 AACCTGTACCGACTGGAAGGGGAGGCTTCTCAGCAATTCCTTGTCTATCAGCACCTTA 1451
QY 461 LeuSerThrGlnGlnProLeuThrLysLysSerGlyValValLeuHisArgAlaValPro 480
DB 1452 CTGAGCACCCAGCAGCCCTCACCAAGAAGAGTGGTGTGCTCGACAGGGCTGTGCC 1511
QY 481 LysAspLysTyrValLeuAsnHisGluAspLeuValLeuGlyGluGlnIleGlyArgGly 500
DB 1512 AAGGACAGTGGTGTCTGAACCATGAGGACCTGGTGTGGTGAGCAGATTGGACGGGG 1571
QY 501 AsnPheGlyGluValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaValLys 520
DB 1572 AACTTTGGCGAAGTGTTCAGCGAGCCCTGCAGCGCGCAACACCCCTGGTGGCGGTGAAG 1631
QY 521 SerCysArgGluThrLeuProProAspLeuLysAlaLysPheLeuGlnGluAlaArgIle 540
DB 1632 TTTTGTGAGAGACGCTCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGGAGATC 1691
QY 541 LeuLysGlnTyrSerHisProAsnIleValArgLeuIleGlyValCysThrGlnLysGln 560
DB 1692 CTGAAGCAGTACAGCCACCCCAACATCGTGTGCTCTCATTTGGTGTCTGCAACCCAGAGCAG 1751
QY 561 ProIleTyrIleValMetGluLeuValGlnGlyGlyAspPheLeuThrPheLeuArgThr 580
DB 1752 CCCATCTACATCGTCATGGAGCTTGTGCAGGGGGGCGCATCTCTGACCTTCTCCCGCAGC 1811
QY 581 GluGlyAlaArgLeuArgValLysThrLeuLeuGlnMetValGlyAspAlaAlaLagly 600
DB 1812 GAGGGGGCCCGCTCGCGGTGAAGACTCTGCTGCAGATGCTGGGGATGCAGCTGTGCG 1871
QY 601 MetGluTyrLeuGluSerLysCysCysIleHisArgAspLeuAlaAlaArgAsnCysLeu 620
DB 1872 ATGGAGTACTTGAGAGCAAGTGTGTCATCCACCCGGGACCTGGCTGCTCGGAACCTCGCTG 1931
QY 621 ValThrLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAlaAsp 640
DB 1932 GTGACAGAGAAGATGCTCTGAAGATCAGTACTTTGGGATGTCCCGAGAGGAGCCGAT 1991
QY 641 GlyValTyrAlaAlaSerGlyGlyLeuArgGlnValProValLysTrpThrAlaProGlu 660
DB 1992 GGGGTCTATGCAGCCTCAGGGGGCCTCAGCAAGTCCCCCGTGAAGTGGACCGCACCTGAG 2051

Qy 661 AlaleuAenTyrGlyArgTyrSerSerGluSerAspValTyrSerPheGlyIleLeuLeu 680
 Db 2052 GCCCTTAACACAGCGCCGCTACTCTCCGAAAGACAGCTGTGGAGCTTTGGCATCTTGCTC 2111
 Qy 681 TrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThrArg 700
 Db 2112 TGGGAGACCTTCAGCCTGGGGCCCTCCCTATCCCAACCTCAGCAATCAGCAGACAGG 2171
 Qy 701 GluPheValGluLysGlyArgLeuProCysProGluLeuCysProAspAlaValPhe 720
 Db 2172 GAGTTTGTGGAGAAGGGGGCCGCTGCTCCCTGCCAGAGCTGTCTCTGATGCCGTGTC 2231
 Qy 721 ArgLeuMetGluGlnCysTyrAlaTyrGluProGlyGlnArgProSerPheSerThrIle 740
 Db 2232 AGGCTCATGGAGCAGTGTGGGCCCTATGAGCCTGGGAGCGGCCAGCTTCAGCACCATC 2291
 Qy 741 TyrGlnGluLeuGlnSerIleArgLysArgHisArg 752
 Db 2292 TACCAGGAGCTGCAGAGCAGTCCGAAAGGGGATCGG 2327

RESULT 2
 US-10-660-763-1
 ; Sequence 1, Application US/10660763
 ; Publication No. US20040063130A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GAN, Weiniu et al.
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: CL001183DIVII
 ; CURRENT APPLICATION NUMBER: US/10/660,763
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: Fast-Seq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 2674
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-660-763-1

Alignment Scores:
 Pred. No.: 0 Length: 2674
 Score: 3879.00 Matches: 752
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 18 Gaps: 0

US-10-660-763-2 (1-752) x US-10-660-763-1 (1-2674)

Qy 1 MetGlyPheSerSerGluLeuCysSerProGlnGlyHisGlyValLeuGlnGlnMetGln 20
 Db 72 ATGGGCTTCTCTTCAGCTGTGTGAGCTCCAGGCCCGCCAGGGGCTCTGCGAAGTGCAG 131
 Qy 21 GluAlaGluLeuArgLeuLeuGluGlyMetArgLysTrpMetAlaGlnArgValLysSer 40
 Db 132 GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCAGCGGGTCAAGAGT 191
 Qy 41 AspArgGluTyrAlaGlyLeuLeuHisHisMetSerLeuGlnAspSerGlyGlnSer 60
 Db 192 GACAGGGAGTATGAGGACTGTCTTCCACCATGTGCTCCGAGGACAGTGGGGGCCAGAGC 251
 Qy 61 ArgAlaIleSerProAspSerProIleSerGlnSerTrpAlaGluIleThrSerGlnThr 80
 Db 252 CGGGCCATCAGCCCTGACAGCCCATCAGTCAGTCTCTGGGCTGAGATCACCAGCCAACT 311
 Qy 81 GluGlyLeuSerArgLeuLeuArgGlnHisAlaGluAspLeuAsnSerGlyProLeuSer 100
 Db 312 GAGGGCCCTGAGCCCTTGTCTGCGGAGCAGCAGCAGAGGATCTGAATCAGGGCCCTCGAGC 371
 Qy 101 LysLeuSerLeuLeuIleArgGluArgGlnGlnLeuArgLysThrTyrSerGluGlnTrp 120
 Db 372 AAGCTGAGCCTGTCTCATCCGGGNAACGGCAGCAGCTTCGCAAGACCTTACAGCGAGCATGG 431

Qy 121 GlnGlnLeuGlnGlnGlnLeuThrLysThrHisSerGlnAspIleGluLysLeuLysSer 140
 Db 432 CAGCAGCTGCAGCAGGAGCTCAACAAGACCACAGCAGGACATTTGAGAAGCTGAAGAGC 491
 Qy 141 GlnTyrArgAlaLeuAlaArgAspSerAlaGlnAlaLysArgLysTyrGlnGlnAlaSer 160
 Db 492 CAGTACCGAGCTCTGGCAGCGGACAGTGGCCCAAGCAAGCGCAAGTACCAAGAGGCGCAGC 551
 Qy 161 LysAspLysAspArgAspLysAlaLysAspLysTyrValArgSerLeuTrpLysLeuPhe 180
 Db 552 AAAGACAAGGACCGTCAAGGCCAAGGACAAGTATGTGGCAGCCTGTGTGAAGCTCTTT 611
 Qy 181 AlaHisHisAsnArgTyrValLeuGlyValArgAlaGlnLeuHisHisGlnHisHis 200
 Db 612 GCTCACCAACAACCGCTATGTCTGGCGTGGCGGCTGCGCAGCTACACCAAGCAGCAC 671
 Qy 201 HisGlnLeuLeuLeuProGlyLeuLeuArgSerLeuGlnAspLeuHisGluGluMetAla 220
 Db 672 CACCAGCTCTCTGCTGCCCGCCCTGCTGCGGTCTACTGAGGACCTGCACGAGAGATGGCT 731
 Qy 221 CysIleLeuLysGluIleLeuGlnGlnTyrLeuGluLysSerSerLeuValGlnAspGlu 240
 Db 732 TGCACTCTGAGGAGATCTCTGAGGAAATACCTGAGATTTAGCAGCCTGTGTGCAAGATGAG 791
 Qy 241 ValValAlaIleHisArgGluMetAlaAlaAlaAlaArgIleGlnProGluAlaGlu 260
 Db 792 GTGGTGGCCATTCAACCGGAGATGGCTGCAGCTGCTGCCGCATCCAGCCTGAGGCTGAG 851
 Qy 261 TyrGlnGlyPheLeuArgGlnTyrGlySerAlaProAspValProProCysValThrPhe 280
 Db 852 TACCAAGGCTTCCTGCGACAGTATGGTTCGCACTGAGCTGCCACCTGTGTGTCAGCTTC 911
 Qy 281 AspGluSerLeuLeuGluGlyGluProLeuGluProGlyGluLeuGlnLeuAsnGlu 300
 Db 912 GATGAGTCACTGCTGAGGAGGGTGAACCGCTGGAGCCTGGGAGCTCCAGCTGAAAGCAG 971
 Qy 301 LeuThrValGluSerValGlnHisThrLeuThrSerValThrAspGluLeuAlaValAla 320
 Db 972 CTGACTGTGGAGAGCTGCAGCACACGCTGACCTCAGTGACAGATGAGCTGGCTGTGGCC 1031
 Qy 321 ThrGluMetValPheArgArgGlnGluMetValThrGlnLeuGlnGlnGlnLeuArgAsn 340
 Db 1032 ACCGAGATGGTGTTCAGGGCGCAGGAGATGGTTTACGAGCTGCAACAGGAGCTCCGGAAT 1091
 Qy 341 GluGluGluAsnThrHisProArgGluArgValGlnLeuLeuGlyLysArgGlnValLeu 360
 Db 1092 GAAGAGGAACACCCACCCCGGAGCGGTGCACTGCTGGGCAAGAGGCAAGTGTCTG 1151
 Qy 361 GlnGluAlaLeuGlnGlyLeuGlnValAlaLeuCysSerGlnAlaLysLeuGlnAlaGln 380
 Db 1152 CAAGAGCAGCTGCAGGGGCTGCAGGTAGCGGTGTCAGCAGCAGGCCAAGCTGCAGGCCAG 1211
 Qy 381 GlnGluLeuLeuGlnThrLysLeuGluHisLeuGlyProGlyGluProProProValLeu 400
 Db 1212 CAGGAGTGTCTGAGCAACAAGCTGGAGCACCTGGGGCCCGCGGAGCCCGCTGTGCTG 1271
 Qy 401 LeuLeuGlnAspAspArgHisSerThrSerSerSerGluGlnGluArgGluGlyArg 420
 Db 1272 CTCCTCGAGATGACCGCACCTCCAGCTGCTCTCGAGCAGGAGGAGGGGGGAAGG 1331
 Qy 421 ThrProThrLeuGluIleLeuLysSerHisIleSerGlyIlePheArgProLysPheSer 440
 Db 1332 ACACCCAGCTGGAGATCTTAAAGCCACATCTCAGGAATCTTCGCCCCCAAGTTCTCG 1391
 Qy 441 AsnLeuTyrArgLeuGluGlyGluGlyPheProSerIleProLeuLeuIleAspHisLeu 460
 Db 1392 AACCTGTACCGACTGGAGGGGAAGGCTTTCCTAGCATTCCTTGTGCTCATCGACCCTA 1451
 Qy 461 LeuSerThrGlnGlnProLeuThrLysLysSerGlyValValLeuHisArgAlaValPro 480
 Db 1452 CTGAGCAGCCAGAGCCCTCCACCAAGAGAGTGGTGTGTCTCTGACAGGGCTGTGGCC 1511

QY 481 LysAspLysTrpValLeuAsnHisGluAspLeuValLeuGluGlnIleGlyArgGly 500
Db 1512 AAGGACAAGTGGGTGTGAACCATGAGACCTGGTGTGGTGAGCAGATTGGACGGGG 1571
QY 501 AsnPheGlyGluValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaVallys 520
Db 1572 AACTTTGGGGAAGTGTTCAGCGGACGCTGCGAGCGCAACACCTGGTGGCGGTGAAG 1631
QY 521 SerCysArgGluThrLeuProAspLeuValAlaValPheLeuGlnGluAlaArgIle 540
Db 1632 TCTTGTGAGAGACGCTCCACCTGACCTCAAGCCCAAGTTTCTCAGGAAGCGAGATC 1691
QY 541 LeuLysGlnTrpSerHisProAsnIleValArgLeuIleGlyValCysThrGlnLysGln 560
Db 1692 CTGAAGCAGTACAGCCACCCACACATCGTGGTCTCTATTGGTGTCTGACCCAGAGCAG 1751
QY 561 ProIleTrpIleValMetGluLeuValGlnGlyAspPheLeuThrPheLeuArgThr 580
Db 1752 CCCATCTACATCTCATGGAGCTTGTGCAAGGGGGGACCTTCCTGACCTTCTCCGCACG 1811
QY 581 GluGlyAlaArgLeuArgVallysThrLeuLeuGlnMetValGlyAspAlaAlaGly 600
Db 1812 GAGGGGGCCGCTGGGGTGAAGATCTGTGTCAGATGTTGGGGGATGCGCTGTGTC 1871
QY 601 MetGluTrpLeuGluSerLysCysCysIleHisArgAspLeuAlaAlaArgAsnCysLeu 620
Db 1872 ATGGAGTACCTGAGAGCAAGTCTGCATCCACCGGACCTGGCTGCTCGGAATGCCTG 1931
QY 621 ValThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAlaAsp 640
Db 1932 GTGACAGAGAAGAATGCTCTGAAGATCAGTGACTTTGGGATGTCCTCGAGAGAGCCGAT 1991
QY 641 GlyValTrpAlaAlaSerGlyGlyLeuArgGlnValProValLysTrpThrAlaProGlu 660
Db 1992 GGGGTCTATGACACCTCAGGGGGCCCTCAGCAAGTCCCCGTGAAGTGAACCGCACCTGAG 2051
QY 661 AlaLeuAsnTrpGlyArgTrpSerSerGluSerAspValTrpSerPheGlyIleLeuLeu 680
Db 2052 GCCCTTAACCTACGGCGCTACTCTCCGAAAGGACGCTGTGGAGCTTTGGCATCTTGCTC 2111
QY 681 TrpGluThrPheSerLeuGlyAlaSerProTrpTrpProAsnLeuSerAsnGlnThrArg 700
Db 2112 TGGGAGACCTTCAGCTGGGGGCTCCCTCCCTATCCCAACCTCAGCAATCAGCAGACCGG 2171
QY 701 GluPheValGluLysGlyArgLeuProCysProGluLeuCysProAspAlaValPhe 720
Db 2172 GAGTTTGTGAGAGGGGGCCGCTGCTGCCCTGCCAGAGCTGTCTGTATGCCGTGTT 2231
QY 721 ArgLeuMetGluGlnCysTrpAlaTrpArgGluProGlyGlnArgProSerPheSerThrIle 740
Db 2232 AGGCTCATGGAGCAGTCTGGGCTATGAGCCTGGGCGGCGCCAGCTTCAGCACCATC 2291
QY 741 TyrGlnGluLeuGlnSerIleArgLysArgHisArg 752
Db 2292 TACGAGAGCTGAGAGCATCCGAAAGCGGCATCGG 2327

RESULT 3

US-10-240-965-256
; Sequence 256, Application US/10240965
; Publication No. US20030165924A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: SHIFFMAN, Dov
; APPLICANT: SOMOGVI, Roland
; APPLICANT: LAWN, Richard M.
; APPLICANT: SEILHAMER, Jeffrey J.
; APPLICANT: PORTER, Gordon J.
; APPLICANT: MIKITA, Thomas
; APPLICANT: TAI, Julie
; TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION
; FILE REFERENCE: PA-0025 PCT
; CURRENT APPLICATION NUMBER: US/10/240,965
; CURRENT FILING DATE: 2002-10-04

; PRIOR APPLICATION NUMBER: 60/195,106
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PERL Program
; SEQ ID NO 256
; LENGTH: 2889
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030165924A1 997347.6
US-10-240-965-256

Alignment Scores:
Pred. No.: 0 Length: 2889
Score: 3821.00 Matches: 752
Percent Similarity: 91.37% Conservative: 0
Best Local Similarity: 91.37% Mismatches: 0
Query Match: 98.50% Indels: 71
DB: 16 Gaps: 1

US-10-660-763-2 (1-752) x US-10-240-965-256 (1-2889)

QY 1 MetGlyPheSerSerGluLeuLeuCysSerProGlnGlyHisGlyValLeuGlnGlnMetGln 20
Db 188 ATGGGCTTCTCTTCTGAGCTGTGACGCCCCAGGGGCCACGGGGTCTCTGCAGCAATGTCAG 247
QY 21 GluAlaGluLeuArgLeuLeuGluGlyMetArgLysTrpMetAlaGlnArgVallysSer 40
Db 248 GAGGCCGAGCTTCGTCTACTGGAGGGCATGAGAAAGTGGATGGCCCGGCTCAAGAGT 307
QY 41 AspArgGluTrpAlaGlyLeuLeuHisMetSerLeuGlnAspSerGlyGlyGlnSer 60
Db 308 GACAGGGAGTATGACGAGTCTTCCACCATGTCTCCAGCAGACAGTGGGGCCAGAGC 367
QY 61 ArgAlaIleSerProAspSerProIleSerGlnSerTrpAlaGluIleThrSerGlnThr 80
Db 368 CGGGCCATCAGCCCTGACAGCCCATCATCTAGTCTCTGGCTGAGATCATCCAGCCAACT 427
QY 81 Glu-GlyLeuSerArgLeuLeuArgGlnHisAlaGluAspLeuAsnSerGlyProLeuSe 100
Db 428 GAGGGCCCTGAGCCCTGCTGGCGCAGCACCGCAGAGGATCTGAACCTAGGGCCCTGAG 487
QY 100 rLysLeuSerLeuLeuIleArgGluArgGlnGlnLeuArgLysThrTyrSerGluGlnTr 120
Db 488 CAAGCTGAGCTTCTCATCCGGAAACGGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTG 547
QY 120 pGlnGlnLeuGlnGlnLeuThrLysThrHisSerGlnAspIleGluLysLeuLysSe 140
Db 548 GAGCAGCTGTCAGCAGGAGCTCACCAGACCACAGCCAGGACATTGAGAACTGAAGAG 607
QY 140 rGlnTrpArgAlaLeuAlaArgAspSerAlaGlnAlaLysArgLysTyrGlnGluAlaSe 160
Db 608 CCAGTACCGAGCTCTGGCAGCGGACAGTCCCAAGCCCAAGCCCAAGTACCAGAGGCCAG 667
QY 160 rLysAspLysAspArgAspLysAlaLysAspLysTyrValArgSerLeuTrpLysLeuPh 180
Db 668 CAAGACAGGACCGTGAACAGCCCAAGGACAAGTATGTACGACGCTCTGGAAGCTCTT 727
QY 180 eAlaHisAsnArgTyrValLeuGlyValArgAlaAlaGlnLeuHisGlnHisHi 200
Db 728 TGCTCACCACAAACCGCTATGTCTGGCGTGGCGGTGGCGAGCTACACCAGCACCA 787
QY 200 shisGlnLeuLeuLeuProGlyLeuLeuArgSerLeuGlnAspLeuHisGluGluMetAl 220
Db 788 CCACCAGCTCTGCTGCCCGGCTGCTGGCTGCTGCGGCTGCGAGCTACACCAGCACCA 847
QY 220 aCysIleLeuLysGluIleLeuGlnGluTyrLeuGluIleSerSerLeuValGlnAspG 240
Db 848 TTGCACTCTGAAGAGATCTCTGAGAAATACCTGGAGATTAGCAGCTCTGTCAGGATGA 907
QY 240 uValValAlaIleHisArgGluMetAlaAlaAlaArgIleGlnProGluAlaG 260

Db 908 GGTGGTGGCCATTACCGGGAGATGGCTGCAGCTGCTGCCGCGATCCAGCTGAGGCTGA 967
Qy 260 uTyrGlnGlyPheLeuArgGlnTyrGlySerAlaProAspValProCysValThrPh 280
Db 968 GTACCAAGGCTTCCTCGACAGATATGGTCCGACCTGACGTCCACCTGTGTCAAGTT 1027
Qy 280 eAspGluSerLeuLeuGluGlyGluProLeuGluProGlyGluLeuGlnLeuAenG 300
Db 1028 CGATGAGTCACTGCTTGGAGGGGTGAACCGCTGGAGCTGGGGAGCTCCAGCTGAACGA 1087
Qy 300 uLeuThrValGluSerValGlnHisThrLeuThrSerValThrAspGluLeuAlaValAl 320
Db 1088 GCTGACTGTGGAGAGCTGCAGACACGCTGACCTCAGTGCAGATGAGCTGGCTGTGGC 1147
Qy 320 aThrGluMetValPheArgGlnGluMetValThrGlnLeuGlnGlnGluLeuArgAs 340
Db 1148 CACCGAGATGGTGTTCAGCGCGCAGGAGATGGTTACGCGAGCTGCAACAGGAGCTCCGAA 1207
Qy 340 nGluGluuAsnThrHisProArgGluArgValGlnLeuLeuGlyLysArgGlnValLe 360
Db 1208 TGAAGAGGAGAACACCCACCCCGGGAGCGGGTGCAGCTGCTGGGCAAGAGGCAAGTGCT 1267
Qy 360 uGlnGluAlaLeuGlnGlnValAlaLeuCysSerGlnAlaLysLeuGlnAlaG 380
Db 1268 GCAAGAGCACTGCGAGGGGCTGCAGGTAGCGCTGTGCAGCAGGCGCAAGCTGCAGGCCCA 1327
Qy 380 nGlnGluLeuGlnThrLysLeuGluHisLeuGlyProGlyGluProProValLe 400
Db 1328 GCAGGAGTTGCTGCAGACCAAGCTGGAGACCTGGGCGCGGAGGCGCCCGCTGTGCT 1387
Qy 400 uLeuLeuGlnAspAspArgHisThrSerSerSerGluGlnGluArgGluGlyArg 420
Db 1388 GCTCTCGAGGATGACCGCACTCCAGCTGCTCTCGAGCAGGAGGAGGGGGGAAG 1447
Qy 420 gThrProThrLeuGluLeuLysSerHisLeuSerGlyLeuPheArgProLysPheSe 440
Db 1448 GACACCCAGCTGAGATCTTAAGAGCCATCTCAGGAATCTTCCGCCCAAGTTCTC 1507
Qy 440 r----- 440
Db 1508 GCTCCCTCCACCGCTGCAGCTCATTCGGAGGTGCAGAGCCCTGCGATGAGCAGCTGTG 1567
Qy 440 ----- 440
Db 1568 GTACCGGGGCCATCCGAGGCGAGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1627
Qy 440 ----- 440
Db 1628 CTTGCTGGGAGAGCAGGCGCAAGAGGAGTACGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1687
Qy 441 -----AsnLeuTy*ArgLeuGluGlyGluGlyPh 450
Db 1688 GCGCGGCACTTCATCATCCAGTCTTGGTAACCTGTACCGACTGGAAGGGAGGCTT 1747
Qy 450 eProSerIleProLeuLeuLeuPheHisLeuLeuSerThrGlnGlnProLeuThrLysLy 470
Db 1748 TCTTAGCATTCCTTGTCTCATCGACCACTACTGAGCAGCAGCAGCAGCAGCAGCAGCAG 1807
Qy 470 sSerGlyValValLeuHisArgAlaValProLysAspLysTrpValLeuAsnHisGluAs 490
Db 1808 GAGTGGTGTGCTGCTGCACAGGGCTGTGCCCAAGGCAAGTGGGTGCTGAACCACTAGGA 1867
Qy 490 pLeuValLeuGluGlnIleGlyArgGlyAsnPheGlyGluValPheSerGlyArgLe 510
Db 1868 CTTGTTGTTGGTGAGCAGATGGACCGGGGAACCTTGGCGAAGTGTTCAGCGGACGCT 1927
Qy 510 uArgAlaAspAsnThrLeuValAlaValLysSerCysArgGluThrLeuProProAspLe 530
Db 1928 GCGAGCGCACAAACCCCTGGTGGCGGTGAAGTCTTGTGAGAGAGCGCTCCACCTGACCT 1987
Qy 530 uLysAlaLysPheLeuGlnGluAlaArgIleLeuLysGlnTyrSerHisProAsnIleVa 550
Db 1988 CAAGGCCAAGTTTCTACAGGAAGCGAGGATCTCGAAGCAGTACAGCCACCCCAACATCGT 2047

Qy 550 lArgLeuIleGlyValCysThrGlnLysGlnProIleTyrIleValMetMetGluLeuValG 570
Db 2048 GCCTCTCATTTGGTGTCTGCACCCAGAGCAGCCCATCTACATGCTCATGGAGCTTGTCA 2107
Qy 570 nGlyGlyAspPheLeuThrPheLeuArgThrGluGlyAlaArgLeuArgValLysThrLe 590
Db 2108 GGGGGGCGACTTCCTGACCTTCCTCGCACGGAGGGGCGCGCTGCGGGTGAAGACTCT 2167
Qy 590 uLeuGlnMetValGlyAspAlaAlaAlaGlyMetGluTyTrLeuGluSerLysCysCyail 610
Db 2168 GCTGCGAGATGGTGGGGATGCAGCTGCTGGCATGGAGTACTGGAGAGCAAGTGTGCAT 2227
Qy 610 eHisArgAspLeuAlaAlaArgAsnCysLeuValThrGluLysAsnValLeuLysIleSe 630
Db 2228 CCACCGGACCTGGCTGCTCGGAACCTGCCTGGTGACAGAGAAGAAATGCTCCTGAAGATCAG 2287
Qy 630 rAspPheGlyMetSerArgGluGluAlaAspGlyValTyTrAlaAlaSerGlyGlyLeuAr 650
Db 2288 TGACTTTGGGATGCTCCGAGAGAGGAGCGGATGGGGTCTATGCAGCCTCAGGGGCGCTCAG 2347
Qy 650 gGlnValProValLysTrpThrAlaProGluAlaLeuAsnTy*GlyArgTyTrSerSerG 670
Db 2348 ACAGTCCCGTGTAGTGGACCGCAGCTGAGGGCGCTTAACCTAGGGCGCTACTCCTCCGA 2407
Qy 670 uSerAspValTrpSerPheGlyIleLeuLeuTrpGluThrPheSerLeuGlyAlaSerPr 690
Db 2408 AAGCAGCTGTGGAGCTTTGGCATCTTGTCTGGAGACCTTCAGCCCTGGGGGCGCTCCCC 2467
Qy 690 oTyrProAsnLeuSerAsnGlnGlnThrArgGluPheValGluLysGlyArgLeuPr 710
Db 2468 CTATCCCAACCTCAGCAATCAGCAGACACGGGAGTTTGTGGAGAAGGGGGCGCTCTGCC 2527
Qy 710 oCysProGluLeuCysProAspAlaValPheArgLeuMetGluGlnCysTrpAlaTyrg 730
Db 2528 CTGCCAGAGCTGTGCTGCTGATGCCGTTCAGGCTCATGGAGCAGTGTCTGGGCTATGA 2587
Qy 730 uProGlyGlnArgProSerPheSerThrIleTyTrGlnGlnLeuGlnSerIleArgLysAr 750
Db 2588 GCCTGGGAGCGGCCCGCAGCTTCAGCACCATCTACCAGGAGCTGCAGAGCATCCGAAAGCG 2647
Qy 750 gHisArg 752
Db 2648 GCATCG 2654

RESULT 4

US-10-003-295-3

; Sequence 3, Application US/10003295

; Publication No. US20020168741A1

; GENERAL INFORMATION:

; APPLICANT: GAN, Weinliu et al.

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: C000183DIV

; CURRENT APPLICATION NUMBER: US/10/003,295

; CURRENT FILING DATE: 2001-12-06

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-003-295-3

Alignment Scores:

Pred. No.:	1,01e-191	Length:	15297
Score:	2137.00	Matches:	747
Percent Similarity:	21.28%	Conservative:	0
Best Local Similarity:	21.28%	Mismatches:	5
Query Match:	55.09%	Indels:	2764
DB:	13	Gaps:	16

[illegible]

Db	6882	GGTGGCATTACCGGGAGATGGCTGCAGCTGTGCCCCGATCCAGCCTGAGGCTAGTA	6941	QY	440	-----	440
QY	261	rGlnGlyPheLeuArgGlnTyr-Gly-	269	Db	8020	CAGCCTGGGCCCCCTACTGTGTGTTCGAGTTTAAATCACTGGGATGCTCTAGAGAGGA	8079
Db	6942	CCAAAGGCTTCCTCGGACAGATATGGTAAGCCCGCTGCTTGTCTCTGCTGGGCCAGGGCT	7001	QY	440	-----	440
QY	270	-----SerAlaProAspValProProc	277	Db	8080	GGCTCTGCCAGGCTGCTTGTATATGGGAAGTTCTCTCTTCCCTGGGATTCACAGGCTGCA	8139
Db	7002	GCTGGCCTGCTCACTGACGGGGCGCTGTCCCCCACAGGTCGGCACCTGACGTCCACACCT	7061	QY	440	-----	440
QY	277	yValThrPheAspGluSerLeuLeuGluGluGluGluProGluGluLeuG	297	Db	8140	GATGTCCCAGACACCTGGCCCCCTGTGACCCCTCCCTTTCCATCGCCCCAGTGTGCTAAAGG	8199
Db	7062	GTGTACGTTCCGATAGTACTGCTTGAGAGGGTGAACCGCTGGAGCCTGGGGAGCTCC	7121	QY	440	-----	440
QY	297	lnLeuAenGluLeuThrValGluSerValGlnHisThrLeu-	310	Db	8200	GACCAGCAACCTCGACTATTCCATGGCTCTCCCTGCTTCAGGAGCGGTTGGGGCCTGTG	8259
Db	7122	AGCTGAACGAGCTGACTGTGTGGAGAGCTGCAGCACACGTG- GGTGGTGGCTTTTGCACCTG	7180	QY	440	-----	440
QY	310	-----	310	Db	8260	GCCTGGAGGAGGAGCACAGCCTTGGTTTGGGGTCTTCCTGCTGGGCTTCCCTTCCCAG	8319
Db	7181	GGCTGGCGGGGCTCCACGACAGACACGAGTGTATTATGTAGCAGGGCTAGTCTGTGA	7240	QY	440	-----	440
QY	310	-----	310	Db	8320	CTCTGCCAGCGTGAGCCTGGGCCAGTCCAGTGCCCATCCAGGGGCTGTGATGGCTC	8379
Db	7241	GACTGTCCAACAGAGCTGTCAACAGGTGGCGGGCTTGTGTGGCTTACAGGGATGCAC	7300	QY	440	-----	440
QY	310	-----	310	Db	8380	TGCATGCCACTCCATGGTTGTAAAGGCTGAGGGCATATAGGGGGAGAGAGACCCCCG	8439
Db	7301	TGGACCTGGGTTGAGGGGGCAGGAGGCTCGGTTCTAATGCTGCCCTTCTCTTGGGTGCA	7360	QY	440	-----	440
QY	311	-----ThrSerValThrAspGluLeuAlaValAlaThrGluMetValPheArgArgGlnG	329	Db	8440	GCTGCCCCCAACGGCCTCTTCAACAAGGTGGTTAAGTGACTCTCTCTCGATCTCTCCCTTG	8499
Db	7361	GGCTGACCTCAGTGACAGATAGCTGGCTGTGGCCACCGAGATGGTGTTCAGGCGCAGG	7420	QY	440	-----	440
QY	329	luMetValThrGlnLeuGlnGluLeuArgAenGluGluAenThrHisProArgG	349	Db	8500	CCAGCTCCCTCCACCGCTGCAGCTCATTTCCGAGGTGCAGAAAGCCCTCGATGAGCAGCT	8559
Db	7421	AGATGGTTACGCAGCTGCAACAGGAGCTCCGGAATGAAGAGAGAACACACCCCGGG	7480	QY	440	-----	440
QY	349	lu-----	349	Db	8560	GTGGTACCACGGGGCCATCCCGAGGGCAGAGGTGGCTGAGTGTGCTGCTGCACTCTGGGGA	8619
Db	7481	AGCGGTGAGTGGGCCCTTGCTGCAGCAGCCTCCTGGGCCCTCCCTCCCTCTACTACCC	7540	QY	440	-----	440
QY	349	-----	349	Db	8620	CTTCTCTGTTGCGGAGAGCAGCGGCAAGCAGGAGTACGTGCTGTCCGTCTCTGTTGGATGG	8679
Db	7541	TAACTGCTGCTAGCCGCCGACAGACCAGCCCTTATTCTTCATCCACCCCTCCACACC	7600	QY	440	-----	440
QY	350	-----ArgValGlnLeuLeuGlyLysArgGlnValLeuGlnGlnAlaLeuGln	365	Db	8680	TCTGCCCCGGCACTTCATCATCCAGTCTTGGATGTGAGTGGGGCTGGGACCCGAGCCCTT	8739
Db	7601	GCCCCCTGCTGCAGGGTGCAGCTGCTGGCAAGAGGCAAGTGTCTCAAGAAGCACTGCAG	7660	QY	440	-----	440
QY	366	GlyLeuGlnValAlaLeuCysserGlnAlaLysLeuGlnAlaGlnGlnLeuLeuGln	385	Db	8740	CCAGGCCTCACTCTTCCCTCCCTTCCCAAGGGAATGGCCTTTTCAGGGTAGGG	8799
Db	7661	GGGCTGCAGGTAGCGCTGTGCAGCAGGCCAAGCTGCAGGCCCCAGCAGGAGTTGCTGCAG	7720	QY	440	-----	440
QY	386	ThrLysLeuGluHisLeuGlyProGlyGluProProValLeuLeuGlnAspAsp	405	Db	8800	GGTAGCTGCCAGGTCTTGGATGCCTCCCTAGCAGGGCTGGTGGAAAGGGGCCACAGAGAC	8859
Db	7721	ACCAAGCTGAGACCTTGGGCCCGCGAGCCCGCGCTGTGTCTCTCTGCTGCTGCAGATGAC	7780	QY	440	-----	440
QY	406	ArgHisSerThrSerSerSer-----	412	Db	8860	CACCCCTGCTCCCTGCAACAAAATAGAGGCTTAAGTGTGAGTCTCCCTCCCTGGTGGGGCAGCA	8919
Db	7781	CGCCACTCCACGTCTCTCTC- GGTGAGCTGCCCCCATCCCGCGCGCGCTGCCCGCACCGGC	7839	QY	440	-----	440
QY	412	-----	412	Db	8920	GGATGTCTATGTGCATCAGATGGCATCTTTTCTGGAGGTCTCTCTGCCCTCTGCTCCCTGGG	8979
Db	7840	CTGCCACCTGGGGCTGCGCTCTCATTTTTCGCCCTCCCTCCCTTAAGCCTGGCCACCC	7899	QY	440	-----	440
QY	413	-----GluGlnGluArgGluGlyArgThrProThrLeu	424	Db	8980	CAGGCCCTTTCTCCCTGTGTCTCTCCCTTCCCTCCCTCCAGGGCTCACGCCCCCTCAGA	9039
Db	7900	GCTGACGTCTGCTCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	7959	QY	441	-----	448
QY	425	GluIleLeuLysSerHisIleSerGlyIlePheArgProLysPheSer-----	440	Db	9040	ATGGAGGCTGTGACCCCGGGTCCCTGCTGCCCTGCTGCAGAACTGTATCCGACTGGAAGGGAA	9099
Db	7960	GAGATCTTAAGAGCCACATCTCAGGAATCTTCGCCCCCAAGTTCTCGGTGAGTGGCGCC	8019				

Qy 449 GlyPheProSerIleProLeuLeuIleAspHisLeuLeuSerThrGlnGlnProLeuThr 468
Db 9100 GGCTTTCTAGCATCTCTTCTCATGACACACTACTGACACCCAGCCCTCCACC 9159
Qy 469 LysLysSerGlyValValLeuHisArgAlaValProLys----- 481
Db 9160 AAGAAAGAGTGGTGTGCTTCTGACAGGGCTGTGCCAAGGTGAGCCTGCACCCAGCCTGG 9219
Qy 481 ----- 481
Db 9220 CCATGCCACCTGTGGCAGGGCTTGGGGAGTGTGGGTGAGGCCACCCAGCGTCTGAGCA 9279
Qy 481 ----- 481
Db 9280 GAAAGGGCTTTCCAGGGCCCTCCGTCTATACAAAGATGACAGTGAAGTGAACCTCAGGGC 9339
Qy 481 ----- 481
Db 9340 CAGCCTTGCTCTAGGTTTGGNAATGTCAGGGCCACTCTCTATGCCATGGCTGTACACACCA 9399
Qy 481 ----- 481
Db 9400 GGTGGTGTCTTACCTGTGTCAGGGCACCTGCCCTGGACCCCGTAGTCATCTCAGTGTGCTCC 9459
Qy 481 ----- 481
Db 9460 CCACGTGTGCCACCCCTGTGTACATATGGAGGGCCCAAAAAATGGAGGACACAGCCCTT 9519
Qy 481 ----- 481
Db 9520 CTAAGGGCCAGCACCCCTTTTCTTTCAGACTTCTGATGCCCTGTCTCTCTTCCCCAG 9579
Qy 482 AspLysTrpValLeuAsnHisGluAspLeuValLeuGlyGlnGlnIleGlyArg----- 499
Db 9580 GACAAGTGGTGTGTAACCATGAGACCTGTGTGGTGTGAGCAGATGGACG-GGTGAG 9638
Qy 499 ----- 499
Db 9639 TGGCCTCTGTGGCTCTTGTGCTGGCGACTTCTCTGAGTCGGCGCTGGGGCCCT 9698
Qy 499 ----- 499
Db 9699 GCCTACACCCAGAAACCTCCCTGCCCCACTGTGATTTCCCCACTTGTACCCGACTCCCT 9758
Qy 499 ----- 499
Db 9759 GCCAGCCCCCACCACACACCATCTCCAGGAAAGGGACAGTACTACGCTGAAACTC 9818
Qy 499 ----- 499
Db 9819 CCAGCAGACAGCTCTGCCAGCACCTGACCTCATCACCCACCCAGGCCGCCCCCATCG 9878
Qy 499 ----- 499
Db 9879 AGCTTTGTGTGCAGCAGGGAGACACCTCTTACTGTAAAGCCATAATACCTGTTTAG 9938
Qy 499 ----- 499
Db 9939 GGAAGAAGTCACTGCTCTAAAATCAGNAATGCTTTTCAAACCCAGGGAGAGTGAATTTT 9998
Qy 499 ----- 499
Db 9999 GGATTTCCATGTCACTTCTCTCAGGAGGGTGGCACATCGGAGGCAACTTTCCCTGCTG 10058
Qy 499 ----- 499
Db 10059 CCCCATGTGCTCTCTAGGTTCCTCCAGCAGGGTCAAACTCCAGAGAGCCTGGGTGGAGG 10118
Qy 499 ----- 499
Db 10119 GGTCCGAACACGGGGGGCCCTCACCCAGGGGTAGGAACAGANTGGGTAGGAAGCGGAGA 10178
Qy 500 -----GlyAsnPhe 502

Db 10179 AGAGAACTCGGGGACTGGGAAGCCCTGTGTAGAGGCCCAAGACCGTTTCAGGGGAACCTT 10238
Qy 503 GlyGluValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaValLysSerCys 522
Db 10239 GGCAGAGTGTTCAGCGGACGCTGCGAGCCGACACACCTGCTGGCGGTGAAGTCTTGT 10298
Qy 523 ArgGluThrLeuProAspLeuLysAlaLysPheLeuGlnGluAla----- 538
Db 10299 CGAGAGACGCTCCACCTGACCTCAAGGCCCAAGTTTCTACAGGAAGCGAGGTGGTGAATA 10358
Qy 538 ----- 538
Db 10359 AACTAATGATCACACGGGTCCCGCATATACAGAGGTTACACTGCATGGCACAGTGTGAA 10418
Qy 538 ----- 538
Db 10419 GTGCTTGACCCAGCGTGGTGTGTTAGTCTCTGAGGCCCCCATTTGGGGGTAGTACCCCC 10478
Qy 538 ----- 538
Db 10479 TTATAGTCCGAAGGGTAGAGGCTGCCCCAGGTACACAGTCCCGGTCTGCTGGCCTTGA 10538
Qy 538 ----- 538
Db 10539 GGCCAAAGCTTCTCCCATCATCTCTGGGGGGCCCTGGGAGGGGGCCCTGGCCACACTAG 10598
Qy 539 -----ArgIleLeuLysGlnTrpSerHisProAsnIleValAr 551
Db 10599 ATCCTGAGCAGCAGTCCCTCCAGGATCTGGAAGCAGTACAGCCACCCCAACATCGTGC 10658
Qy 551 gLeuIleGlyValCysThrGlnLysGlnProIleTrpIleValMetGluLeuValGln-- 570
Db 10659 TCTCATTTGGTGTCTGACCCAGAGCAGCCCATCTACATCTCATGTGAGGCTTGTGACGG 10718
Qy 570 ----- 570
Db 10719 TGAGCGGGGGCGCTGAGTCTCAGGTAGGGCGCGCAGCTGTGTGAGTGGCAGCTTACC 10778
Qy 571 -----GlyGlyAspPheLeuThrPheLeuAr 579
Db 10779 TCAGGAGGCTCAGCAGGGGTCTCTCCCACTTGAGGGGGCGACTTCTCTGACCTTCTCCG 10838
Qy 579 gThrGluGlyAlaArgLeuArgValLysThrLeuLeuGlnMetValGlyAspAlaAla 599
Db 10839 CACGAGGGGGCCCGCTGCGGGTGAAGACTCTGTGCAGATGTGTGGGGATGAGCTGC 10898
Qy 599 aGlyMetGluTrpLeuGluSerLysCysCysIleHisArg----- 612
Db 10899 TGGCATGGAGTACTCTGGAGAGCAAGTGTGCTCATCCACCG-GTGAGTGGCGGTGGCCACG 10957
Qy 612 ----- 612
Db 10958 GGCCCTGCCAACACCCCGGACCAGAGTCAAGAGGTACTATACCCCTAGGGCCCCCGCT 11017
Qy 612 ----- 612
Db 11018 GGACCATCAGGCATCAGCTCCAGAGGGGGAGTTGGCTCTGTGTAGACAGGGGTGCCCA 11077
Qy 612 ----- 612
Db 11078 GGCCCGGGAGCAGCTTTTGTCTTGGCTTTCCTAGAGTGTTCAGCCAGGGCTGGGAGGC 11137
Qy 613 -----AspLeuAlaAlaArgAsnCy 619
Db 11138 GACTGTTGGCAATGAGCCCTGCCCTGTCTCACCCAGGGACCTGGCTGCTCGGAACCTG 11197
Qy 619 aLeuValThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAl 639
Db 11198 CTTGGTGACAGAGAGAAATGCTCTGAAGATCACTGACTTTGGGATGTGCCAGAGGAAGC 11257
Qy 639 aAspGlyValTyAlaAlaSerGlyGlyLeuArgGlnValProValLysTrpThrAlaPr 659
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Db	11258	CGATGGGGCTCTATGTCAGCCTCAGGGGGCCTCAGACAAGTCCCGGTGAAGTGGACCGCGACC	11311
Qy	659	oGluAlaLeuAsnTyr----- 	664
Db	11318	TGAGGCCCTTAACTACGGTACCTAGTCCCTGTCTACCTCGACTCCATGGCCAGAGGCCA	11377
Qy	664	-----	664
Db	11378	GGCCTGGGTCTGCGGCTGCTCGCCCTGGCCCCAGGAGGGTGCACCTCAGCTGGCCTC	11437
Qy	665	-----GlyArgTyr--SerSerGluSerAspValTrpSerPheGlyI 	678
Db	11438	ACCTCCTCGCCTCTCTGTCAGGGCGCTACTCTCTCCGAAAGCGACGTGTGGAGCTTTGGCA	11497
Qy	678	leLeuLeuTrpGluThrPheSerLeuGlyAlaSerProTyrProhenLeuSerAenGlnG	698
Db	11498	TCCTGTCTCTGGAGACCTTCAGCGCTGGGGCCTTCCCTCTATCCCAACCTCAGCAATCAGC	11557
Qy	698	lnThrArgGluPheValGluLys----- 	705
Db	11558	AGACAGGGAGTTTGTGGAGAGGGTAAGCACCTGTGATGACAGCAGCCTCAGGCTGCA	11617
Qy	705	-----	705
Db	11618	CCCTCTTCAGATGCTCCAGCGGACTCTTCTAACTCCTTAAATGCAACCTTCCACCA	11677
Qy	705	-----	705
Db	11678	GGCAGAAATAGAATAAACCCTGGCCAGTTGCTCAGCGCTGTATCCAGCAGCTTTGGGAGGC	11737
Qy	705	-----	705
Db	11738	TGAGCTGGGTGGATCACTTGAGCCAGGAGTTCAGAGTCAGCTTGGACAAACACAGTGA	11797
Qy	705	-----	705
Db	11798	CTCCATCTGTACAAAAAATAACAAAAATAGACTGGGCACGGTGGCTCACACCTGTAATCCC	11857
Qy	705	-----	705
Db	11858	AGCACTTTGGGAGCCGAGGCAGGTGGATCACTGTGGTCAGGAGTTTGAGACCAGCCAG	11917
Qy	705	-----	705
Db	11918	ACCAACATGGTGAACCCCATCTCTACTAAAAATACAAAAATTAGCCAGCATGTGGCA	11977
Qy	705	-----	705
Db	11978	CGTCCCTGTAAATCCCAGCTACTTTGGGAGGCTGAGTGGGAGAAATTGCTTGAACCCAGAG	12037
Qy	705	-----	705
Db	12038	GCGGAGGCTGCAGTGAGCCGAGATTGTGCCACTGCACCTCCAGCCTGGGCGACAAGAGTGA	12097
Qy	705	-----	705
Db	12098	AACTCCATCTCAAAAAAACCAAAAAACAAAAAATACAAAAATTAGTGGGTGTGGTGAC	12157
Qy	705	-----	705
Db	12158	ATGCGCTGTAGTCCCTGTACTCTGGGAGGCTGAGTGGGAGGATCACTGGAGCCCGGA	12217
Qy	705	-----	705
Db	12218	GGTGGAGGTTGAGTGAGCTGAGATCATGCCACTGCACCCCAACCTGGGTGACAGAGAGA	12277
Qy	705	-----	705
Db	12278	GAGAGACCTTGACTCGAAAAAGAAAAAAACCTGGGGCAGTGGCTCAGCGCTGAATT	12337
Qy	705	-----	705
Db	12338	TCAACATTTTGGGAGGCTGAGGAGGTGGATCACTTGAGCTTAGGAGTTTGACACTAGCC	12397

RESULT 5

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US-10-660-763-3
; Sequence 3, Application US/10660763
; Publication No. US20040063130A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE
; TITLE OF INVENTION: ACID MOLECULES ENCOD
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIVII
; CURRENT APPLICATION NUMBER: US/10/660,763
; CURRENT FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.1.0
; SEQ ID NO 3
; LENGTH: 15297
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-660-763-3

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Alignment Scores:		
Pred. No.:	1,01e-191	Length: 15297
Score:	2137.00	Matches: 747
Percent Similarity:	21.28%	Conservative: 0

Best Local Similarity: 21.28% Mismatches: 5
Query Match: 55.09% Indels: 2764
DB: 18 Gaps: 16

US-10-660-763-2 (1-752) x US-10-660-763-3 (1-15297)

Qy	1	MetClyPheSerSerGluLeuCySerProGlnGlyHisGlyValLeuGlnMetGln	20
Db	2563	ATGGGCTTCTCTCTAGCTGTGCAGCCCGCCAGGGCCACGGGGTCTTGCACGAATGCAG	2622
Qy	21	GluAlaGluLeuArgLeuGluGlyMetArgLysTrpMetAlaGlnArgValLysSer	40
Db	2623	GAGGCCAGCTTCTCTACTGGAGGCATGAGAAAGTGGATGGCCAGCGGGTCAAGAT	2682
Qy	41	AspArgGluTyAlaGlyLeuLeuHisMetSerLeuGlnAepSerGlyGlnSer	60
Db	2683	GACAGGAGTATGCAGGACTGCTTCCACCATGTCCTCGCAGGACAGTGGGGGCCAGAGC	2742
Qy	61	ArgAlaIleSerProAepSerProIleSerGlnSer	72
Db	2743	CGGGCCATCAGCCCTGACAGCCCATCAGTCAGGT-GGGTCTCTATGGGACTCTGTGGG	2801
Qy	72	-----	72
Db	2802	TGCTGGCGTATCTGCCCTTCTCCTCTCTCTGGGGGCCCTCTGGGGCAGTGGCTGGAGA	2861
Qy	72	-----	72
Db	2862	TCTGGCAGGCAATGCTTGGAGCCATTGTGCCCCCTCCTCGCTCCCCCATCTGTGCT	2921
Qy	73	-----TrpAlaGluIleThrSerGlnThrGluGlyLeuSerArgLeuLeuArgGln	89
Db	2922	GTATAGTCTCTGGGCTGAGATCACAGCCAACTGAGGGCTGAGCCGCTTGTCTGGGCAG	2981
Qy	90	HisAlaGluAepLeuAenSerGlyProLeuSerLysLeuSerLeuLeuIleArgGluArg	109
Db	2982	CACGACAGGATCTGAATCAGGGCCCTGAGCAGCTGAGCTGCTCATCCGGGAACGG	3041
Qy	110	GlnGlnLeuArgLysThrTySerGluGlnTrpGlnGlnLeuGlnGluLeuThrLys	129
Db	3042	CAGCAGCTTCGCAAGACCTACAGCGAGCAGTGGCAGCAGCTGCAGCAGGAGCTCACCAAG	3101
Qy	129	-----	129
Db	3102	GTGAGCGGCGAGCAGCTGGGGCTTGGGTCAATTTCTGTCTAAATTTTGAGCCTCGAAGGGGT	3161
Qy	129	-----	129
Db	3162	TGTTTTGCACAAGAGGCCCTGGATTCACTGGGGAAGTGTAAATCCCTGACCGCAGGCGCTG	3221
Qy	129	-----	129
Db	3222	GCTTGCTTAACCTTGATGTAGCTTCTCTCTTCTTCCCTAGCTTGGCTGGCTGCA	3281
Qy	129	-----	129
Db	3282	GCAAGGCTCTCTGTGCTTTTTTCTGTGCTGGCCAAAGTGTGGGAGTGAAGATGAGT	3341
Qy	129	-----	129
Db	3342	GACCGGTCACTGCTGGGAGAGCTCAGAAATCGGTACTCGCTCCACACTGTGGCCATCT	3401
Qy	129	-----	129
Db	3402	GGCTCTGGGTCTCAGAGTCAGGGAGAGGAATGAGGGTCAGTCTGTTTGGCTTCGACCTA	3461
Qy	129	-----	129
Db	3462	TGCAGCTCTCTCAGGGGCCAGAGACTGGGAGCAGCATGGCCCCCGAAGGTTCGAGG	3521
Qy	129	-----	129
Db	3522	ACTCGGGCCGTGAAGTCAGCCTGCTAGGTTTGAATCCCAAGCTCCTCAGTCTTAGAG	3581

Qy	129	-----	129
Db	3582	GCTGTGTGATTTGGAAACTATTATCTGGAGGCTAGTGGCCCAATTCAGTGTCTGTGTC	3641
Qy	129	-----	129
Db	3642	CCCTCCTGCACACACCCCTTCTCAAGTGCAGAGCCCGCCCTTGGCATGGACCCACAG	3701
Qy	129	-----	129
Db	3702	CGSCCCTGTGTGGCCACCCCTGGGCCCATTCCTCGCCCCAAAAGATCATCTGATTCAAGGG	3761
Qy	129	-----	129
Db	3762	TGGGCCCATTTTATAAGTTTGTCTGGAACACAGCATATGCCCTTTGTTTTCATATTGT	3821
Qy	129	-----	129
Db	3822	CTGTGACTACAATGACAGAGTTGAGTAAATTGTGACAGAGGCTCTATGGCCTACAAGCCTA	3881
Qy	129	-----	129
Db	3882	AAATATTTTACTATCTGGCCCTTTAAGAAAAAGACTGATCTAGTCGAGGAATCTAGC	3941
Qy	129	-----	129
Db	3942	TCAGTTACAGATGGGAAACTGAGGTTGGCGCTTGGCCAAACATATCCAGCACATAAAC	4001
Qy	129	-----	129
Db	4002	AGGAGAACTGGGACGAGAAACACTGATCTCGGGCTGTCACTATTCTTACTGTCCCAAGACA	4061
Qy	129	-----	129
Db	4062	TAATTTTCAGGACCCAGTGCAAAGTCAAATTTGTGGGGTCTTTGTTTAAAGATTGTCTAGG	4121
Qy	129	-----	129
Db	4122	AATTTCCAGTGGCAATAATGAGAAATGAACCAAGCACAGGGCCCTTCTACATGTGGAG	4181
Qy	129	-----	129
Db	4182	CCCCGTGTGACTGCACAGGCGGTGCACACTGCACCTGGCCCTGCCTGCCACCAGGCTAC	4241
Qy	129	-----	129
Db	4242	CAGTGTCACTCCNAAGAGGGGACCGTTGTAGCCTGTAGTCTACCTCTTTGCCTCCCCAAGG	4301
Qy	129	-----	129
Db	4302	GGTCTGTCTTCAACAGGCTCTCTGATCTTTGACTCTCAGCTCAGCAGCAGCTTTCCAG	4361
Qy	129	-----	129
Db	4362	AAGTCTCCAGGTGCTCTTCCCTGCAGCAGGACCTTTTCAGGGCTTCACCCAGGCAAG	4421
Qy	130	-----ThrHi	131
Db	4422	AATCTTCCAACTGGGGACCTGCTGCCCCACACTGGCCCTCTCTCTCTCTAGACCCA	4481
Qy	131	sSerGlnAepIleGluLysLeuLysSerGlnTyArgAlaLeuAlaAArgAepSerAlaGl	151
Db	4482	CAGCCAGGACATTTAGAAAGCTGAAGAGCCAGTACCAGAGCTCTGGCACGGGACAGTGCCA	4541
Qy	151	nalAlaLysArgLysTyGlnGluAlaSerLys	161
Db	4542	AGCCAAAGCGCAAGTACCAGGAGGCCAGCAAGGTTTCGTGGCTTCCCTTGTGTCAGGGAG	4601
Qy	161	-----	161
Db	4602	GGNATCCGAAGCCAGTGTGACTGCTTCTTGGGTACCCAGAGAGTGGGGGCTGCTGGGC	4661

441 -----AsnLeuTyrArgLeuGluGlyGlu 448
441 Db
9040 ATGGAGGCTGCTGACCCCGGGTCCCTGCGCTGCGAGAACTGTACCGACTGGAGGGGAA 9099
449 GlyPheProSerIleProLeuLeuIleAspHisLeuLeuSerThrGlnGlnProLeuThr 468
449 Db
9100 GGCTTTCCTAGCATTCCTTTGGCTCATCGACCACTACTGAGCACCCAGAGCCCTCACC 9159
469 LysGlySerGlyValValLeuHisArgAlaValProIys----- 481
469 Db
9160 AAGAAAGAGTGGTGTGTGCTGCGCAGGGCTGTGCCCAAGGTGAGCTGCACCCAGCCCTGG 9219
481 ----- 481
481 Db
9220 CCGATGCCACCTGTGGCAGGGCTTGGGGAGTGTGGGTGTCAGGCCCAACCCAGCGTCTGAGCA 9279
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9280 GAAAGGGCTTTCCAGGGCCCTCCGTCTACATACAAGATGCAGAGTGAGTGACCCCTCAGGGC 9339
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9340 CAGCCTTGCTCTAGTTTGAATGTGAGGCCCACTCCTATGCCATGGGCTGTACACCA 9399
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482 AspLysTrpValLeuAsnHisGluAspLeuValLeuGlyGlnIleGlyArg----- 499
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9999 GGATTTTCATGTCACTTCTCTCAGGAAGGGTGGCAGCATCGGAGGCAACTTTCCTGCTG 10058
499 ----- 499
499 Db
10059 CCCCATGTGCTCTAGTGTCTCCAGCGAGGGTCAAACTCCACAGAGACCTGGGTGGAGG 10118
499 ----- 499

10119 GGTCCGAACACAGGGGGCCCCCTCACCCAGGGGTAGGAAGCAGAATGGTAGGAAGCGGAGA 10178
500 -----GlyAsnPhe 502
10179 AGAGAACTCGGGGACTGGGAAGCGCGTGTAGGAGCCCAAGACCCGTTTCAGGGGACCTTT 10238
503 GlyGluValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaValLysSerCys 522
503 Db
10239 GCGAAGTGTTCAGGGGAGCGCTGCGAGCCGACACACCTGGTGGCGGTGAAGTCTTGT 10298
523 ArgGluThrLeuProAspLeuLysAlaLysPheLeuGlnGluAla----- 538
523 Db
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538 ----- 538
538 Db
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538 ----- 538
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538 Db
10539 GGCCAAGCTCTTCTCCCATCATCCTCGGGGGCCCTGGGAGCGGCGCTGCCACGTAG 10598
539 -----ArgIleLeuLysGlnTyrSerHisProAsnIleValAr 551
10599 ATCTTGAGCAGCAGTGCCTCCAGGATCTGAAGCAGTACAGCCACCCCAACATCGTGG 10658
551 GLeuIleGlyValCysThrGlnLysGlnProIleValMetGluLeuValGln-- 570
10659 TCTCATTTGTGTCTGCACCAGAGCGCCATCTACATCTGTCATGGAGCTGTGCGAGG 10718
570 ----- 570
570 Db
10719 TGAGCGGGGGCGCTCAGCTCCAGGTAGGGCGCGAGCCCTGTCAGTGGCAGCCTTACC 10778
571 -----GlyGlyAspPheLeuThrPheLeuAr 579
10779 TCAGGAGGCTCAGCAGGGGTCTCCACCTCGAGGGGGCGACTTCTCAGCTCTCTCCG 10838
579 GThrGluGlyAlaArgLeuArgValLysThrLeuLeuGlnMetValGlyAspAlaAla 599
10839 CACGAGGGGGCGCGCTCGGGGTGAAGACTCTGTCGAGATGGTGGGGGATGCAGCTGC 10898
599 aGlyMetGluTyrLeuGluSerLysCysCysIleHisArg----- 612
10899 TGGCATGGAGTACTGGAGAGCAAGTGTCTGCATCCACCG-GTGAGTGGCGGTGGCCACG 10957
612 ----- 612
612 Db
10958 GGCCCTGCCAACACACCCCGACAGAGTCAAGAGGTACCTATACCCCTAGGGCCCCCGCT 11017
612 ----- 612
612 Db
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612 ----- 612
612 Db
11078 GGSCCGGAGAGCTTTTGTCTTGGCTTTCTAGAGTGTTCAGCCAGGGCTGGGCGAGC 11137
613 -----AspLeuAlaAlaArgPheCys 619
11138 GACTGTTGGCCAAATAGCCCCCTGCCCCCTGTCTCCAGGGACCTGGCTCTCGAACTG 11197
619 sLeuValThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluAla 639
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Db 11198 CCTGGTACAGAGAAGATGCTCTGAAGATCAGTGCATCTTTGGGATGTCCCGAGAGGAAGC 11257
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Db 11258 CGATGGGCTCTATGCGAGCTCAGGGGCTCAGACAAGTCCCGCTGAAGTGGACCGCAC 11317
Qy 659 oGluAlaLeuSerTyr----- 664
Db 11318 TGAGGCCCTTAACGTACGTACTAGTCCCTGTCTACCCGTGACTCCATGGCCAGAGGCCA 11377
Qy 664 ----- 664
Db 11378 GGCCTGGGTCTGCGGGTGCCTCGCCCTGCGCCCGAGGGGGTGCACTACGCTGCCTC 11437
Qy 665 -----GlyArgTyrSerSerGluSerAspValTyrSerPheGlyI 678
Db 11438 ACCTCCTCGCCTCCTGTCAGGGCGCTACTCCTCGAAAGCGACGTGTGGAGCTTTGGCA 11497
Qy 678 leLeuLeuTyrGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnG 698
Db 11498 TCTTGCTCTGGGAGACCTTCAGCCTGGGGGCTCCCGCTATCCCAACCTCAGCAATCAGC 11557
Qy 698 InThrArgGluPheValGluLys----- 705
Db 11558 AGACAGGGAGTTTGTGGAGAAGGGTAAGCAACCTGTGATGACAGAGCCCTCAGGCTGCA 11617
Qy 705 ----- 705
Db 11618 CCCTCTTCAGATGCTCCAGCGGACTCTTCTTAACCTCCCTTAATGCCAACCTTCCACCA 11677
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Db 11678 GGCAGATAAGATAAACCTGCGCAGTTGCTCAGCGCTGTATCCCGACACTTTTGGAGGC 11737
Qy 705 ----- 705
Db 11738 TGAGCTGGTGGATCACTTTGAGCCCGAGAGTTCAAGATCAGCTTGGACAACACAGTAAA 11797
Qy 705 ----- 705
Db 11798 CTCCATCTGTACAAAAAATACAAAAATAGACTGGGCAGCGTGGCTCACACCTGTAATCCC 11857
Qy 705 ----- 705
Db 11858 AGCACTTTGGAGGCCGAGGAGGTGATCACCTGTGTCAGGAGTTTGGACAGCCAG 11917
Qy 705 ----- 705
Db 11918 ACCAACATGTGAACCCCATCTCTACTAAAAATACAAAAAATTAGCCAGGCGATGGTGCA 11977
Qy 705 ----- 705
Db 11978 CGTGCCTGTATCCAGCTACTTTGGGAGGTGAGGTGGGAGAATTGCTTGAACCCAGGAG 12037
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Db 12038 GCGGAGGCTGAGTGCAGCCGAGATTGTGCCACTGCACCTCCAGCCTGGCGCACAGAGTGA 12097
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Db 12158 ATGCGCTGTAGTCCCTGCTACTCGGAGGCTGAGGTGGGAGGATCACTGGAGCCCGGGA 12217
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Db 12218 GGTGGAGTTGCAGTGAGCTGAGATCATGTCACCTGCCACCCCAACCTGGTGACAGAGAGA 12277
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Db 12278 GAGAGACCTTGACTCGAAAAAGAAAAAACCCTGGGCGCAGTGGCTCAGCCCTGTAATT 12337

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Db 12398 TGCCCAACATGCGCAAAACCTGTCTCTACTAAAAAATACAAAAAATTAGCGAGGTGTAGTG 12457
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Db 12518 AGGTGAGGTTGCAGTGAGCTGAGATCACACCACTGCATTCAGCGTGGGTGACAGAGCA 12577
Qy 705 ----- 705
Db 12578 AGACTCCATCTCAGAAAAAAGAAAAAATAAGAAATATCCCTGTAGCTACTACTAGTG 12637
Qy 705 ----- 705
Db 12638 AGCACCTGGTCTGTGTAGTGCATGTATTTTCATTTGCTCATCTACATGTGTGGTA 12697
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Db 12698 GGGATTAATATGTCCTTTCTCAGATGGAATAACAGCTGGCAGAGGGGACACAGCTAGC 12757
Qy 705 ----- 705
Db 12758 ACCTGGTAGGATTAGGATCAGAACCCAGGCTCTTTTGTCTTTGGGCCCTTTGGTGGAGAA 12817
Qy 705 ----- 705
Db 12818 CAGTGATCCTTCAGAACAGTGATCTTAAGCAGCTCCTATGCTCATGTATGCTATCCCCCAG 12877
Qy 705 ----- 705
Db 12878 AGTCTGCCGAGGACCTCAAACTCCCTCATGCTGTGTGCTGTGCTCTCTCTCACA 12937
Qy 706 GlyGlyValArgLeuProCysProGluLeuCysProAspAlaValPheArgLeuMetGluGln 725
Db 12938 GGGGGCGTCTGCCCTGCCCGAGAGCTGTCTCTGATGCCGTGTTCAGGCTCATGGAGCAG 12997
Qy 726 CysTrpAlaTyrGluProGlyGlnArgProSerPheSerThrIleTyrGlnGluLeuGln 745
Db 12998 TGCTGGCCTATGAGCTGGGCGAGCGGCCAGCTTTCAGCACCATCTTACCAGGAGCTGCAG 13057
Qy 746 SerIleArgLysArgHisArg 752
Db 13058 AGCATCCGAAAGCGGCATCGG 13078

RESULT 6
US-10-887-553A-240
; Sequence 240, Application US/10887553A
; Publication No. US20050085436A1
; GENERAL INFORMATION:
; APPLICANT: Garza, Dan
; APPLICANT: Li, Hao
; TITLE OF INVENTION: Method to treat conditions associated
; FILE OF INVENTION: with insulin signalling dysregulation
; FILE REFERENCE: 4-33262
; CURRENT APPLICATION NUMBER: US/10/887,553A
; PRIOR FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: 60/485,883
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 240
; LENGTH: 2950
; TYPE: DNA
; ORGANISM: human
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US-10-887-553A-240									
Alignment Scores:									
Pred. No.:	1.1e-165	Length:	2950						
Score:	1853.00	Matches:	376						
Percent Similarity:	63.60%	Conservative:	150						
Best Local Similarity:	45.47%	Mismatches:	217						
Query Match:	47.77%	Indels:	84						
DB:	21	Gaps:	9						
US-10-660-763-2 (1-752) x US-10-887-553A-240 (1-2950)									
QY	1	MetGlyPheSerSerGluLeuLeuCysSerProGlnGlyHisGlyValLeuGlnGlnMetGln	20						
DB	385	ATGGGGTTTGGAGTACCTG-----AAGAATTTCATGAGCAGTGTAAATTTGCAA	438						
QY	21	GluAlaGluLeuArgLeuLeuGluGlyMetArgLysTrpMetAlaGlnArgValLysSer	40						
DB	439	GACTGGGAATTACGGTTACTGGAAACAGTAAGAAATTTATGGCCCTGAGAAATAAAAGT	498						
QY	41	AspArgGluTyrAlaGlyLeuLeuHisHisMetSerLeuGlnAspSerGlyGlyGlnSer	60						
DB	499	GATAAAGATATGATCTACTTTCAGAAACCTTTGTAATCAAGTTGATAAGGAAAGTACT	558						
QY	61	ArgAlaIleSerProAspSerProIleSerGlnSerTrpAlaGluIleThrSerGlnThr	80						
DB	559	GTCCAAATGAATATGTCAGCAACGTATCCAAGTCTTGGCTACTTATGATTCAGCAGACA	618						
QY	81	GluGlyLeuSerArgLeuLeuArgGlnHisAlaGluAspLeuAsnSerGlyProLeuSer	100						
DB	619	GAACAACTTAGTAGGATAATGAAGACACATGCAGAGGACTTGAACCTCTGGACCTTTACAC	678						
QY	101	LysLeuSerLeuLeuIleArgGluArgGlnGlnLeuArgLysThrTyrSerGluGlnTrp	120						
DB	679	AGGCTCACCATGATGATTAAAGCAACGACGAGGTGAAGAAAGTTACATAGTGTTCAT	738						
QY	121	GlnGlnLeuGlnGlnGluLeuThrLysThrHisSerGlnAspIleGluLysLeuLysSer	140						
DB	739	CAGCAGATAGAGGCAGAGATGATCAAGGTTACCAAAACAGAAATTTGGAGAAAGTTAAATGC	798						
QY	141	GlnTyrArgAlaLeuAlaArgAspSerAlaGlnAlaLysArgLysTyrGlnGluAla---	159						
DB	799	AGCTATAGACAATTAATAAAGAAATGAATTTCTGCCAAAGAGAAATATAAAGAGCTTTA	858						
QY	160	SerLysAspLysAspArgAspLysAlaLysAspLysTyrValArgSerLeuTrpLysLeu	179						
DB	859	GCTAAAGGAGGAACTCAAAAGGCCCAAGCAAGCATACGCAAGCCACCAATGAAACTT	918						
QY	180	PheAlaHisAsnArgTyrValLeuGlyValArgAlaAlaGlnLeuHisGlnHis	199						
DB	919	CATATGTTGCACAAATCAGTATGATTGGCGTTGAAAGGGGCACAGCTCCATCAGAAATCAG	978						
QY	200	HisHisGlnLeuLeuLeuProGlyLeuLeuArgSerLeuGlnAspLeuHisGluGluMet	219						
DB	979	TATTATGATATCACACTTCCCTGCTTCTGGACTCCTTACAAAGAGATGCAAGAAAGATG	1038						
QY	220	AlaCysIleLeuLysGluLeuGlnGlnTyrLeuGluIleSerSerLeuValGlnAsp	239						
DB	1039	ATAAAGCACTCAAGGTATATTTGATGATATACAGCCAGATAACCGACTTGTTCACAGAG	1098						
QY	240	GluValValAlaIleHisArgGluMetAlaAlaAlaAlaArgIleGlnProGluAla	259						
DB	1099	GAATAGTGAATGTCATCAAAAGAGATTCAAATGTCCGTTGCAACAGATAGATCCTAGTACA	1158						
QY	260	GluTyrGlnGlnPheLeuArgGlnTyrGlySerAlaProAspValProCysValThr	279						
DB	1159	GAATACAAATAATTTATAGATGTTTTCAGAACCAACCGCTGCTAAAGAACAGAAATAGAG	1218						
QY	280	PheAspGluSerLeuLeuGluGlyGluProLeuGlnProGlyGluLeuGlnLeuAsn	299						
DB	1219	TTTGATCTCTCTACTGGAAGAAATGAAATCTTTCAGGCAAAATGAGATCATGTGGAAT	1278						
QY	300	GluLeuThrValGluSerValGlnHisThrLeuThrSerValThrAspGluLeuAlaVal	319						

DB	1279	AACTTAACAGCAGAAAGTTTGGCAAGTAATGTTGAAAACGTTTAGCGGAAGAACTTATGCAA	1338
QY	320	AlaThrGluMetValPheArgArgGlnGlnMetValThrGlnLeuGlnGlnLeuLeuArg	339
DB	1339	ACACAGCAGATGCTTTTAAACACAGGAGGAGCGTGTGTGGAGTTAGAGAGAAGAAATGAA	1398
QY	340	AsnGluGluGlnAsnThrHisProArg---GluArgValGlnLeuLeuGlyLysArgGln	358
DB	1399	GAATCTTCTGAAACTTGTGAGAAAGTCTGATATTGTGCTTCTGCTAAGCCAAACACAG	1458
QY	359	ValLeuGlnGlnAlaLeuLeuGlnGlyLeuGlnValAlaLeuCysSerGlnAlaLysLeuGln	378
DB	1459	GCATTGGAAGAACTGAAACAGTCAGCTCAGCAGCTGAGATGCACTGAAGCAAAAGTTTCA	1518
QY	379	AlaGlnGlnGluLeuLeuGlnThrLysLeuGluHisLeuGlyProGlyGluProProPro	398
DB	1519	GCACAGAAAGAAATTACTAGACCAAAAGTGCAGAAATGATGGGAAGAGCCACTCCA	1578
QY	399	ValLeuLeuLeuGlnAspArgHisSerThrSerSerGluGlnGlnGluArgGluGly	418
DB	1579	GTAGTAAATTTATGAAGAAGATGCAGATCAGTTACATCTATGGAAGAAAGAGAG-	1632
QY	419	GlyArgThrProThrLeuGluLulleuLysSerHisIleSerGlyIlePheArg---Pro	437
DB	1633	---AGGCTATCCAAATTTGAATCTATTCTGTCATTCAATTTGCTGGAATATTAGGTCTCCA	1689
QY	438	Lys-----	438
DB	1690	AAATCTGCAGTGGGCTCTTCAGCACCTTTCTGATATGATCTCCATCAGTGAGAAGCCTTTG	1749
QY	438	-----	438
DB	1750	GCAGAACAGACTGGTACCATGGTCAATTTCCAGATATAGAAAGCTCAAGAACTGTTAAAA	1809
QY	438	-----	438
DB	1810	AAACAAGGAGACTTTTGGTGCAGAGAGTCAATGGGAAACCTGGTGAATATGCTCTTTCT	1869
QY	439	-----	439
DB	1870	GTATATTTCTGATGGACAGAGGAGACATTTTATCATACAATATGTTGATAACATGATCGA	1929
QY	445	LeuGluGlyGluGlyPheProSerIleProLeuLeuIleAspHisLeuLeuSerThrGln	464
DB	1930	TTTCGAGGCACTGGGTTTCAACATCTCCTCAACTTATAGATCATCATACACAAAA	1989
QY	465	GlnProLeuThrLysLysSerGlyValValLeuHisArgAlaValProLysAsp---Lys	483
DB	1990	CAGGTATCATCAAGAAATCAGGTGTGTTCTGCTGAAATCTTCTTCTAAGGACAAGAAA	2049
QY	484	TrpValLeuAsnHisGluAspLeuValLeuGlyGluGlnIleGlyArgGlyAsnPheGly	503
DB	2050	TGGATTTCTCAGTCATCAAGATGTCTATTTGGGAGAAATTAATGGGCAAGGAAATTTTGGT	2109
QY	504	GluValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaValLysSerCysArg	523
DB	2110	GAAGTATATAAGGCGCACATTAAG---GATAAACTCTTCTGTTGCTTAAACATGTAAA	2166
QY	524	GluThrLeuProProAspLeuLysAlaLysPheLeuGlnGlnAlaAlaArgIleLeuLysGln	543
DB	2167	GAAGATCTTCTCAGGAAATGAAAAATAAAATTTTACAAAGAGCCAAAAATTTCTCAAGCA	2226
QY	544	TyrSerHisProAsnIleValArgLeuIleGlyValCysThrGlnLysGlnProIleTyr	563
DB	2227	TATGATCATCCCAATATTGTCAAACTTATAGGAGTTTGCACAAAGACAGACCTGTCTAC	2286
QY	564	IleValMetGluLeuValGlnGlyGlyAspPheLeuThrPheLeuArgThrGlyGlyAla	583
DB	2287	ATCATTTGGAACCTGGTTTTCAGGAGGTGATTTCTCCTCACTTTCTGAGAAGAGAAAGAT	2346
QY	584	ArgLeuArgValLysThrLeuLeuGlnMetValGlyAspAlaAlaAlaGlyMetGluTyr	603

Db 2347 GAACTAAACCAACAGTTAGTGAATTTTCATTAGACGCTGCTGCTGGTATGTTGTAT 2406
Qy 604 LeuGluSerLysCysCysIleHisArgAspLeuAlaAlaArgAsnCysLeuValThrGlu 623
Db 2407 CTCGAGAGTAAAAACTGTATACACAGGACCTTGCTGCAAGAAATCGCTCGTAGGTGAA 2466
Qy 624 LysAsnValLeuIleSerAspPheGlyMetSerArgGluGluAlaAspGlyValTyr 643
Db 2467 AATATGTTCTTGAAATCAGTGACTTTTGGAAATGCTCGTCAAGAGGATGGTGGAGTGTAT 2526
Qy 644 AlaAlaSerGlyGlyLeuArgGlnValProValLysTrpThrAlaProGluAlaLeuAsn 663
Db 2527 TCATCTTCT---GGCTTAAGCAGATTCCTTAAATGAGCAGCACCAGGAAGCTCTTAAT 2583
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Db 2584 TATGGAGATACAGTTCAGAGAGTGACGTGTGGAGCTTTGGCATCTTCTCTGGGAGACC 2643
Qy 684 PheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnThrArgGluPheVal 703
Db 2644 TTCAGCTTAGGGGTTTGTCCGTACCTCGGAATGACAAATCAGCAAGCAAGAGCAAGTA 2703
Qy 704 GluLysGlyGlyArgLeuProCysProGluLeuCysProAspAlaValPheArgLeuMet 723
Db 2704 GAAAGAGATACCGGATGTCAGCTCCCGCAGCAGTGTCCAGAGGATATTTCCAAATCATG 2763
Qy 724 GluGlnCysTrpAlaTyrGluProGlyGlnArgProSerPheSerThrIleTyrGlnGlu 743
Db 2764 ATGAAGTGTGGGATTATAAACCCTGMAAATCGCCCTAAGTTTCAGTGAACCTTCAGAAAGAG 2823
Qy 744 LeuGlnSerIleArgLysArg 750
Db 2824 CTCACATCATCAAGAGAAAA 2844

RESULT 7

US-10-280-576-19
; Sequence 19, Application US/10280576
; Publication No. US2004004405A1
; GENERAL INFORMATION:
; APPLICANT: Wolff, Matthew R.
; TITLE OF INVENTION: VASCULAR STENT OR GRAFT COATED OR IMPREGNATED WITH PROTEIN
; FILE REFERENCE: 09820.189
; CURRENT APPLICATION NUMBER: US/10/280.576
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 60/343,732
; PRIOR FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1779
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-280-576-19

Alignment Scores:
Pred. No.: 1,78e-74 Length: 1779
Score: 892.00 Matches: 222
Percent Similarity: 51.35% Conservative: 83
Best Local Similarity: 37.37% Mismatches: 185
Query Match: 23.00% Indels: 105
DB: 18 Gaps: 13

US-10-660-763-2 (1-752) x US-10-280-576-19 (1-1779)

Qy 197 HisGlnHisHisHis-----GlnLeuLeuLeuPro 206
Db 159 CAGGATCACCACCATTAACACTACACTACACGACGCGCTCCAGGAAAACTCAAG 218
Qy 207 GlyLeuLeuArgSerLeuGlnAspLeuHisGlu-----GluMetAlaCysIleLeu 223
Db 219 ACTGAAATTCAAAGTGCCCAAGATCCAGAGAAATCAAGAGCCATCCGCATACATTCG 278
Qy 224 LysGluIleLeuGlnGluTyrLeuGluIleSerSerLeuValGlnAspGluValAla 243

Db 279 CTCCAAGTTCTCTCAATTTCCAGTTTGAAGCCCTCCAAGCCCGTGCAA-----ACA 326
Qy 244 IleHisArgGluMetAlaAlaAlaAlaAla-ArgIleGlnProGluAlaGluTyrGlnG 263
Db 327 GTGCACCAAGAG-----ACGTCGCATCCATCCCGACCAAAAGTGCTTTGA 371
Qy 263 yPheLeuArgGlnTyr-----GlySerAlaProAsp----- 273
Db 372 TTTTGCACAAAGAGTTCCAGGTGGAACACACCGGTGGTTCCGCGCGCGATGAGCAATTCGT 431
Qy 274 -----ValProCysValThrPheAspGluSerLe 284
Db 432 CAACTGTCCGCCAGCTGTCAAAAGCCTGTTAAGCCATCCGTCCAAATATATCCGGC----- 486
Qy 284 uLeuGluGluGluGluProLeuGlu-----ProGlyGluLeuGlnLeuAsn---GluLe 301
Db 487 -----CACAAAGATCACCCGTTCCAGTCCAGTTCCTGGAGAGCTGGACGAGAATCCGATCG 542
Qy 301 uThrValGluSerValGlnHisThrLeuThrSerValThrAspGluLeuAlaValAlaTh 321
Db 543 GGACATCGACACACGACGAGGAGGAGGAGGATAGCGCCAGCTGACGACGCTGTCTCAGCATCAA 602
Qy 321 rGluMetValPheArgArgGlnGluMetValThrGlnLeuGlnGlnGluLeuArgAsn-- 340
Db 603 GGATCACTGCTATTTGGCTGCCAGCCTGGCGGCAGTATATCGCTCTCCACAAATCGTCC 662
Qy 341 -----GluGluGluAsnThrHis-----ProArgGluArgValGlnLeuLeuG 355
Db 663 GCTTTACGAGAGGAGATGTTTCCATGGCGTCTTCGCCGCGGAGGAAGTG----- 711
Qy 355 yLysArgGlnValLeuGlnGluAlaLeuGlnGlyLeuGlnValAlaLeuCysSerGlnAl 375
Db 711 ----- 711
Qy 375 aLysLeuGlnAlaGlnGlnLeuLeuGlnThrLysLeuGluHisLeuGlyProGlyG 395
Db 711 ----- 711
Qy 395 uProProProValLeuLeuLeuGlnAspArgHis-SerThrSerSerSerGluGlnG 415
Db 712 -----GTTCCGATTGCTGAATACGATGGTGACTTCTCGTCCGCAAAAGCATTCG 761
Qy 415 luArgGluGlyArgThrProThrLeuGluLeuLeuLysSerHisIleSerGlyIleP 435
Db 762 AAAAGAGGAGAGCCAGATTGTGCTCAGTGTCTGTGAATGGCCATAAGCACTTCATTGT 821
Qy 435 heArgProLysPheSerAsnLeuTyrArgLeuGluGlyGluGlyPheProSerIleProL 455
Db 822 CCAGACCCACCGGA-GAGGGTAAATTTCCGGTTCGAGGAGCCACCATTTCGCCAGCATCCAGG 880
Qy 455 euLeuIleAspHisLeuLeuSerThrGlnGlnProLeuThrLysLysSerGlyValVal 475
Db 881 AGCTGATCATCATCAGTATCATCTCGGAATTCAGTCAGTCGCGTGAATTCGGAGCCATAC 940
Qy 475 euHisArgAlaValProLysAspLysTrpValLeuAsnHisGluAspLeuValLeuGlyG 495
Db 941 TCCGACGACCCCGTTTCGCGGAGCGCTGGAGCTGAGCAACGATGATGTGTACTTCTGG 1000
Qy 495 luGlnIleGlyArgGlyAsnPheGlyGluValPheSerGlyArgLeuArgAlaAspAsnT 515
Db 1001 AGAGGATTGGTCGGGGAACCTTTGGGGATGTCTACAAAGGCCAACCTGAAGTCCACCAAAC 1060
Qy 515 hrLeuValAlaValLysSerCysArgGluThrLysLeuProProLeuLeuAlaLysPheL 535
Db 1061 TGGATGTGGCTGTCAAAACCTGTGAGTACCTTCGCGCGAGCAACAGACGCTAAATTC 1120
Qy 535 euGlnGluAlaArgIleLeuLysGlnTyrSerHisProAsnIleValArgLeuIleGlyV 555
Db 1121 TACAGAAAGGGCGCATCCTCAAGCAATACGATCATCCAAATATCGTAAATTTGATTGGCA 1180
Qy 555 alCysThrGlnLysGlnProIleTyrIleValMetGluLeuValGlnGlnGlyAspPheL 575

Db 1181 TTTGTGTGCAGAACGCCCATCATGATTGTCATGGAATTGGTGTGCTCGTGTTCGCTTT 1240
Qy 575 euThrPheLeuArgThrGluGlyAlaArgLeuArgVallyThrLeuLeuGlnMetValG 595
Db 1241 TAACTATTATACCAAGAACTCCATGGCTCTACCACTGCCCAACAATGGCGATGTGCA 1300
Qy 595 lyAspAlaAlaGlyMetGluThrLeuGluSerLysCysCysIleHisArgAspLeuA 615
Db 1301 GAGATGGCGGCGAGGATCGGATATCTGGAGTCCAAAACTGCATTCATCGCATCTGG 1360
Qy 615 laAlaArgAsnCysLeuValThrGluLysAsnValLeuLysIleSerAspPheGlyMets 635
Db 1361 CGGCGCGTAATGTCTCGTTGACTTGGAGCAGAGTGTGAAGATCTCCGATTTCGGAATGT 1420
Qy 635 erArgGluGluAlaAspGlyValTyraAlaSerGlyGlyLeuArgGlnValProValL 655
Db 1421 CTCCGAGGAGAGGAA-----TATATAGTTTCCGATGGCATGAAACAATACCTGTGA 1474
Qy 655 ySTrPThrAlaProGluAlaLeuAsnTyrglyArgTyrsSerSerGluSerAspValTIPS 675
Db 1475 AGTGACAGCTCCCGAGGCGCTTGAATTCGGCAAGTACACTTCGTTGTGGCATGTGTGT 1534
Qy 675 erPheGlyIleLeuLeuTIPGluThrPheSerLeuGlyAlaSerProTyProAsnLeuS 695
Db 1535 CCTATGGCATACTGATGTGGAGATCTTCTCCAAGGCGCACACACCTACTCCGGCATGA 1594
Qy 695 erAsnGlnInThrArgGluPheValGluLysGlyArgLeuProCysProGluLeuC 715
Db 1595 CCAACTCCAGAGCAGAGCGCATCGATACGGGATATCGTATGCCAACCGCGAAGAGCA 1654
Qy 715 ySTrPThrAlaValPheArgLeuMetGluGlnCysTrpAlaTyrgluProGlyGlnArgP 735
Db 1655 CGCCGAGGAGATGTACCGATGATGTCTCAGTCTCGGAGCGCGCGAATCCCGAC 1714
Qy 735 roSerPheSerThrIleTyrglnGluLeuGlnSerIle 747
Db 1715 CGCATTTTCGATGAGATCTACAATGGTGGTGCATGCTG 1752

RESULT 8
US-09-918-995-1503
; Sequence 1503, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1503
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(449)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-1503

Alignment Scores:
Pred. No.: 1,64e-53 Length: 449
Score: 663.00 Matches: 136
Percent Similarity: 80.47% Conservatives: 0
Best Local Similarity: 80.47% Mismatches: 0
Query Match: 17.09% Indels: 33
DB: 10 Gaps: 1

US-10-660-763-2 (1-752) x US-09-918-995-1503 (1-449)

Qy 511 ArgAlaAspAsnThrLeuValAlaVallySerCysArgGluThrLeuProProAspLeu 530
Db 39 CGAGCGAGCAACACCCCTGGTGGCGGTGAAGTCTTGTGAGAGACGCTCCACCTGACCTC 98
Qy 531 LysAlaLysPheLeuGlnGluAlaArgIleLeuLysGlnTyrsHisProAsnIleVal 550
Db 99 AAGCCCAAGTTTCTACAGGAAGCGAGG----- 125
Qy 551 ArgLeuIleGlyValCysThrGlnLysGlnProIleTyriLeValMetGluLeuValGln 570
Db 125 ----- 125
Qy 571 GlyGly-AspPheLeuThrPheLeuArgThrGluGlyAlaArgLeuArgVallyThrLe 590
Db 126 ---GGCGACTTCTCGACCTTCTCTCCGACGAGGGGGCCCGCTGCGGGTGAAGACTCT 182
Qy 590 uLeuGlnMetValGlyAspAlaAlaIAGlyMetGluTyrluGluSerLysCysCysI 610
Db 183 GCTGCAGATGGTGGGGATGCAGCTGCTGGCATGGAGTACCTGGAGAGCAAGTCTGCTGCAT 242
Qy 610 eHisArgAspLeuAlaAlaArgAsnCysLeuValThrGluLysAsnValLeuLysIleSe 630
Db 243 CCACCGGACTTGGCTGCTCGGAACCTGCTGTGCAGAGAGAAGTATGCTCTGAAGATCAG 302
Qy 630 rAspPheGlyMetSerArgGluGluAlaAspGlyValTyraAlaSerGlyGlyLeuAr 650
Db 303 TGACTTTGGGATGTCCCGAGAGAGCGGATGGGGTCTATGCAGCCTCAGGGGGCTCAG 362
Qy 650 gGlnValProVallySTrPThrAlaProGluAlaLeuAsnTyrglyArgTyrsSerGl 670
Db 363 ACNAGTCCCGTGAAGTGGACCGCACCTTAGGCCCTTAACCTACGGCGCTACTCTCTCGA 422
Qy 670 uSerAspValTrpSerPheGlyIle 678
Db 423 AAGCGACGTGTGGAGCTTTTGGCATC 447

RESULT 9

US-10-204-041-3
; Sequence 3, Application US/10204041
; Publication No. US20030176443A1
; GENERAL INFORMATION:
; APPLICANT: STEIN-GERLACH, MATTHIAS
; APPLICANT: SALASSIDIS, KONSTADINOS
; APPLICANT: BACHER, GERALD
; APPLICANT: MULLER, STEFAN
; TITLE OF INVENTION: Pyridylpyrimidine Derivatives as Effective Compounds Against Prion
; TITLE OF INVENTION: Infections and Prion Diseases
; FILE REFERENCE: AXM-007.1P US
; CURRENT APPLICATION NUMBER: US/10/204,041
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: EP 01111858.5
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: PCT/EP02/05420
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3840
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-204-041-3

Alignment Scores:
Pred. No.: 1.58e-48 Length: 3840
Score: 624.50 Matches: 138
Percent Similarity: 53.79% Conservatives: 68
Best Local Similarity: 36.03% Mismatches: 128
Query Match: 16.10% Indels: 49
DB: 16 Gaps: 10

US-10-660-763-2 (1-752) x US-10-204-041-3 (1-3840)

Qy 405 AspArgHisSerThrSerSerSerGluGlnGluArgGlyGlyArgThrProThrLeu 424

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Db 731 GAGAAACACTCTCGGTACCATGGCCGCTGTGTCGCCGAATGCCGCTGAGTATCCG----- 784
Qy 425 GluIleLeuYsSerHisIleSerGlyIlePheArgProLysPheSer----- 440
Db 785 -----CTGAGCAGCGGGATCAATGGCAGCTTCTTGGTGGTGAGAGTGAGAGCAGTCCT 838
Qy 440 ----- 440
Db 839 AGCCAGAGTCCATCTCGCTGAGATACGAAGGAGGGGTGTACCATTTACAGGATCAACACT 898
Qy 441 -----AsnLeuTyrArgLeuGluGlyGluGlyPheProSerIleProLeuLeu 456
Db 899 CTTTCTGATGCAAGCTCTAGCTCTCTCCGAGAGCCGCTTCAACACCCCTGGCGGAGTTG 958
Qy 457 IleAspHis-----LeuLeuSerThr-----GlnGlnProLeuThr 468
Db 959 GTTCATCATCATCAACGGTGGCCGACGGGCTCATCACCAGCTCCATTCACAGCCCCA 1018
Qy 469 LysLysSerGlyValValLeuHisArgAlaValProLys---AspLysTrpValLeuAsn 487
Db 1019 AAGCGCAACAGCCACTGTCTATGGTGTGTCTCCCACTACGACAAAGTGGAGATGGAA 1078
Qy 488 HisGluAspLeuValLeuGlyGluGlnIleGlyArgAsnPheGlyGluValPheSer 507
Db 1079 CGCAGGACATCACCATGAGACACAAGCTGGCGGGCCAGTACGGGGAGGTGTACGAG 1138
Qy 508 GlyArgLeuArgAlaAspAsnThrLeuValAlaValLysSerCysArgGlu---ThrLeu 526
Db 1139 GCGTGTGGAGAATACAGCCTGACGGTGGCCGTGAAGACCTTGAAGGAGGACCATCATG 1198
Qy 527 ProProAspLeuLysAlaLysPheLeuGlnGluAlaArgIleLeuLysGlnTyrSerHis 546
Db 1199 GAGGTGGAA-----GAGTTCTGAAAGAGCTGCAGTCAATGAAAGAGATCAAAAC 1249
Qy 547 ProAsnIleValArgLeuIleGlyValCysThrGlnLysGlnProIleTyrIleValMet 566
Db 1250 CCTAACCTAGTGCAGCTCTTGGGGTGTGCACCGGAGCCCGCTTCTATATCATCACT 1309
Qy 567 GluLeuValGlnGlyArgPheLeuThrPheLeuArgThrGluGlyAlaArgLeuArg 586
Db 1310 GAGTTTCATGACCTACGGGACCTCTGGACTACTCTGAGG---GAGTGCACCGGACGAG 1366
Qy 587 ValLys-----ThrLeuLeuGlnMetValGlyAspAlaAlaLaglyMetGluTyrLeu 604
Db 1367 GTGAACGCGGTGTGCTGTATATGCGCCACTCAGATCTCGTCAGCCATGGAGTACCTA 1426
Qy 605 GluSerLysCysCysIleHisArgAspLeuAlaAlaArgAsnCysLeuValThrGluLys 624
Db 1427 GAGAGAGAAATCTTCATCCACAGAGATCTTCTGCTGCCGAAACTGCTGGTAGGGGAGAAC 1486
Qy 625 AsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAlaAspGlyValTyrAla 644
Db 1487 CACTTGTGAAGTAGCTGATTTGGCTGAGCAGGTGTGATCAGCGGGACACCTACACA 1546
Qy 645 AlaSerGlyLeuArgGlnValProValLysTrpThrAlaProGluAlaLeuAsnTyr 664
Db 1547 GCCCATGTGGAGCAAG---TTCCCATCAATGGACTGCACCCGAGAGCTGGCCTAC 1603
Qy 665 GlyArgTyrSerSerGluSerAspValTrpSerPheGlyIleLeuLeuTrpGluThrPhe 684
Db 1604 AACAAGTTCTCCATCAAGTCCGAGCTCTGGGCATTTGGAGTATTTGCTTGGGAAATTTGCT 1663
Qy 685 SerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThrArgGluPheValGlu 704
Db 1664 ACCTATGGCATGTCCCTTACCCGGGAATGACCGTTCCAGGTGTATGAGCTCTAGAG 1723
Qy 705 LysGlyGlyArgLeuProCysProGluLeuCysProAspAlaValPheArgLeuMetGlu 724
Db 1724 AAGGACTACCGCATGACGAGCGCCAGAGGCTGCCAGAGAGGCTTATGAACCTCATCGGA 1783
Qy 725 GlnCysTrpAlaTyrGluProGlyGlnArgProSerPheSerThrIleTyrGlnGluLeu 744
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Db 1784 GCATGTTGGCAGTGGAAATCCCTCTGACCGGCCCTCTTTGCTGNAATCCACCAAGCCTTT 1843
Qy 745 GlnSerIle 747
Db 1844 GAAACAATG 1852

RESULT 10
US-10-717-597-234
; Sequence 234, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dörner, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 234
; LENGTH: 3840
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-234

Alignment Scores:
Pred. No.: 1,58e-48 Length: 3840
Score: 624.50 Matches: 138
Percent Similarity: 53.79% Conservative: 68
Best Local Similarity: 36.03% Mismatches: 128
Query Match: 16.10% Indels: 49
DB: 19 Gaps: 10

US-10-660-763-2 (1-752) x US-10-717-597-234 (1-3840)
Qy 405 AspArgHisSerThrSerSerGluGlnGluArgGlyGlyArgThrProThrLeu 424
Db 731 GAGAAACACTCTCGGTACCATGGCCGCTGTGTCGCCGAATGCCGCTGAGTATCCG----- 784
Qy 425 GluIleLeuLysSerHisIleSerGlyIlePheArgProLysPheSer----- 440
Db 785 -----CTGAGCAGCGGGATCAATGGCAGCTTCTTGGTGGTGAGAGTGAGAGCAGTCCT 838
Qy 440 ----- 440
Db 839 AGCCAGAGTCCATCTCGCTGAGATACGAAGGAGGGGTGTACCATTTACAGGATCAACACT 898
Qy 441 -----AsnLeuTyrArgLeuGluGlyGluGlyPheProSerIleProLeuLeu 456
Db 899 CTTTCTGATGCAAGCTCTAGCTCTCTCCGAGAGCCGCTTCAACACCCCTGGCGGAGTTG 958
Qy 457 IleAspHis-----LeuLeuSerThr-----GlnGlnProLeuThr 468
Db 959 GTTCATCATCATCAACGGTGGCCGACGGGCTCATCACCAGCTCCATTCACAGCCCCA 1018
Qy 469 LysLysSerGlyValValLeuHisArgAlaValProLys---AspLysTrpValLeuAsn 487
Db 1019 AAGCGCAACAGCCACTGTCTATGGTGTGTCTCCCACTACGACAAAGTGGAGATGGAA 1078
Qy 488 HisGluAspLeuValLeuGlyGluGlnIleGlyArgAsnPheGlyGluValPheSer 507
Db 1079 CGCAGGACATCACCATGAGACACAAGCTGGCGGGCCAGTACGGGGAGGTGTACGAG 1138
Qy 508 GlyArgLeuArgAlaAspAsnThrLeuValAlaValLysSerCysArgGlu---ThrLeu 526
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Alignment Scores:		1,59e-48	Length:	3840
Pred. No.:	Score:	624.50	Matches:	138
Percent Similarity:		53.79%	Conservative:	68
Best Local Similarity:		36.03%	Mismatches:	128
Query Match:		16.10%	Indels:	49
DB:		19	Gaps:	10
US-10-660-763-2 (1-752) x US-10-802-432-26 (1-3840)				
QY	405	AspArgHisSerThrSerSerSerGluGlnGluArgGluGlyArgThrProThrLeu	424	
DB	731	GAGAAACACTCTCTGGTACCATCGGCTGTGTCCTCCCAATGCCGTGAGTATCCG	784	
QY	425	GluileLeuLysSerHisIleSerGlyIlePheArgProLysPheSer	440	
DB	785	CTGAGCAGCGGGATCAATGGCAGCTTCTTGGTGCCTGAGAGTGAGAGCAGTCTCT	838	
QY	440	AGCCAGAGGTCCATCTCGCTGAGATACGAGGAGGGTGTACCATTTACAGGATCAACACT	898	
DB	839	AGCCAGAGGTCCATCTCGCTGAGATACGAGGAGGGTGTACCATTTACAGGATCAACACT	898	
QY	441	AsnLeuTyrArgLeuGluGlyGluGlyPheProSerIleProLeuLeu	456	
DB	899	GCTTCTGATGGCAAGCTCTACGCTCTCTCCGAGAGCGGCTTCAACACCTGCGCGAGTTG	958	
QY	457	IleAspHis	468	
DB	959	GTTTCATCATATTCAACGGTGGCGGAGCGGCTCATCCACAGCTCCATTTATCGAGCCCCA	1018	
QY	469	LysLysSerGlyValValLeuHisArgAlaValProLys	487	
DB	1019	AAGCGCAACAGCCACTGTCTATGGTGTGTCTCCCACTACGACAGTGGGAGATGGAA	1078	
QY	488	HisGluAspLeuValLeuGlyGluGlnIleGlyArgGlyAsnPheGlyGluValPheSer	507	
DB	1079	CGCAGCGACATCACCATGAAGCAGCAGCTGGGCGGGGCCAGTAGTACGGAGGTGTACGAG	1138	
QY	508	GlyArgLeuArgAlaAspAsnThrLeuValAlaValLysSerCysArgGlu	526	
DB	1139	GGCGTGTGAAGAATAATCAGCTGACGCTGGCGTGGCGCTGGAAGACCTTGAAGGAGGACACCATG	1198	
QY	527	ProProAspLeuLysAlaLysPheLeuGlnGluAlaArgIleLeuLysGlnTyrSerHis	546	
DB	1199	GAGGTGGAA	1249	
QY	547	ProAsnIleValArgLeuIleGlyValCysThrGlnLysGlnProIleTyrIleValMet	566	
DB	1250	CCTAACCTAGTCAGCTCTTGGGTCTGCACCCGGGAGCCCCGCTTCTATATCATCACT	1309	
QY	567	GluLeuValGlnGlyAspPheLeuArgThrPheLeuArgThrGluGlyAlaArgLeuArg	586	
DB	1310	GAGTTCATGACCTACCGGAACCTCTCGACTACCTGAGG	1366	
QY	587	ValLys	604	
DB	1367	GTGAACGCCCTGTGCTGTCTGTACATGGCCACTCAGATCTCGTCAGCCATGAGTACCTTA	1426	
QY	605	GluSerLysCysCysIleHisArgAspLeuAlaAlaArgAsnCysLeuValThrGluLys	624	
DB	1427	GAGNAGAAAACCTTCTCCACAGAGATCTTGTCTGCCGAACTGCTGTGGTGGGAGAAC	1486	
QY	625	AsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAlaAspGlyValTyrAla	644	
DB	1487	CACCTTGTGAAGTAGCTGATTTGGCTTGACGAGGTTGATGACAGGGGACACCTACACA	1546	
QY	645	AlaSerGlyGlyLeuArgGlnValProValLysTyrThrAlaProGluAlaLeuAsnTyr	664	
DB	1547	GCCCATGCTGGAGCCAG	1603	
QY	665	GlyArgTyrSerSerGluSerAspValTyrPheGlyIleLeuLeuTyrPhe	684	
DB	1604	AACAGTTCTCCATCAAGTCCGACGTCTGGGCAATTTGGAGTATTTGCTTTGGGAAATGCT	1663	

RESULT 11
US-10-802-432-26
; Sequence 26, Application US/10802432
; Publication No. US20040185489A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Transcriptional Activity Assay
; FILE OF INVENTION: 21574
; CURRENT APPLICATION NUMBER: US/10/802,432
; CURRENT FILING DATE: 2004-03-17
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 3840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: proto-oncogene tyrosine-protein kinase c-abl
; LOCATION: (1)-(3840)
; OTHER INFORMATION: GenBank accession No. M14752
US-10-802-432-26


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Qy 685 SerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnThrArgGluPheValGlu 704
Dy 1664 ACCTATGGCATGTCCCTTACCCGGGAATTACCGGTTCCTCCAGGTGTATGAGCTGTAGAG 1723
Qy 705 LysGlyGlyArgLeuProCysProGluLeuCysProAspAlaValPheArgLeuMetGlu 724
Dy 1724 AAGGACTACCGATGAGCGCCAGAGGTCGCCAGAGAGGTCTATGAACCTATGCGGA 1783
Qy 725 GlnCysTrpAlaTyrGluProGlyGlnArgProSerPheSerThrIleTyrGlnGluLeu 744
Dy 1784 GCATGTTGGCAGTGGAAATCCCTCTGACCGGCGCTCTCTTGTGTAATCCACCAAGCCTTT 1843
Qy 745 GlnSerile 747
Dy 1844 GAAACAATG 1852

RESULT 12
US-10-170-385-182
; Sequence 182, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 53268200100
; CURRENT APPLICATION NUMBER: US/10/170.385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 5434
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-170-385-182

Alignment Scores:
Pred. No.: 2.58e-48 Length: 5434
Score: 624.50 Matches: 138
Percent Similarity: 53.79% Conservative: 68
Best Local Similarity: 36.03% Mismatches: 128
Query Match: 16.10% Indels: 49
DB: 17 Gaps: 10

US-10-660-763-2 (1-752) x US-10-170-385-182 (1-5434)
Qy 405 AspArgHisSerThrSerSerGluGlnGluArgGluGlyArgThrProThrLeu 424
Dy 421 GAGAAACACTCTCGTACCATGGCGCTGTGTCGCCGAATGCCGCTGATATCCG----- 474
Qy 425 GluIleLeuYsSerHisIleSerGlyIlePheArgProLysPheSer----- 440
Dy 475 -----CTGACGCGGGATCAATGGCAGCTTCTTGTGGCTGAGAGAGAGTCTCT 528
Qy 440 ----- 440
Dy 529 AGCCAGAGGTCCATCTCGCTGAGATACGAGAGGAGGTGTACCATTCAGGATCAACACT 588
Qy 441 -----AsnLeuTyrArgLeuGluGlyGluGlyPheProSerIleProLeuLeu 456
Dy 589 GCTTCTGATGCAAGCTCTACGTCTCTCTCCGAGAGCGCGCTTCAACACCCCTGGCGAGTTG 648
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Qy 457 IleAspHis-----LeuLeuSerThr---GlnGlnProLeuThr 468
Dy 649 GTTCATCATCATTTCAACGGTGGCGGCGGCTCATCACCGCTCCATTTATCCAGCCCCA 708
Qy 469 LysLysSerGlyValValLeuHisArgAlaValProLys---AspLysTyrValLeuAsn 487
Dy 709 AAGCGCAACAGCCCATCTGTATGTGTGTCTCCCACTACGACAACTGGGATCGGAGTGA 768
Qy 488 HisGluAspLeuValLeuGlyGluGlnIleGlyArgGlyAsnPheGlyGluValPheSer 507
Dy 769 CGCACGGACATCACCATGAAGCAACAGCTGGCGGGGGCCAGTACGGGGAGGTGTACGAG 828
Qy 508 GlyArgLeuArgAlaAspAsnThrLeuValAlaValLysSerCysArgGlu---ThrLeu 526
Dy 829 GCGCTGTGGAAGAAATACAGCCTGACGGTGGCGGTGAAGACCTTGAAGAGGAGCACCATG 888
Qy 527 ProProAspLeuLysAlaLysPheLeuGlnGluAlaArgIleLeuLysGlnTyrSerHis 546
Dy 889 GAGGTGGAA-----GAGTCTTTGAAGAGAGCTGACATCATGAAGAGATCAACAC 939
Qy 547 ProAsnIleValArgLeuIleGlyValCysThrGlnLysGlnProIleTyrIleValMet 566
Dy 940 CCTAACCTAGTCAGCTCTCTTGGGCTGTGCACCGGAGGCCCGTTCATATCATCACT 999
Qy 567 GluLeuValGlnGlyGlyAspPheLeuThrPheLeuArgThrGluGlyAlaArgLeuArg 586
Dy 1000 GAGTTTCATGACCTACCGGAACCTCTCGACTACTCTGAGG---GAGTGCAACCGGACGAG 1056
Qy 587 ValLys-----ThrLeuLeuGlnMetValGlyAspAlaAlaGlyMetGluTyrLeu 604
Dy 1057 GTGAAGCCCGTGTGTCTGTATCATGGCCACTCAGATCTCGTCGCGCATGGAGTACTTA 1116
Qy 605 GluSerLysCysCysIleHisArgAspLeuAlaAlaArgAsnCysLeuValThrGluLys 624
Dy 1117 GAGAAGAAAACCTTCATCCACAGAGATCTTGCTGCCGAAACTGCCTGGTAGGGGAGAAC 1176
Qy 625 AsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAlaAspGlyValTyrAla 644
Dy 1177 CACTTGGTGAAGGTAGCTGATTTTGGCCTGAGCAGGTTGATGACAGGGGACACCTACACA 1236
Qy 645 AlaSerGlyGlyLeuArgGlnValProValLysTrpThrAlaProGluAlaLeuAsnTyr 664
Dy 1237 GCCCATGCTGGAGCCAAG---TTCCCATCAATGGACTGCACCCGAGAGCTGGCTTAC 1293
Qy 665 GlyArgTyrSerSerGluSerAspValTrpSerPheGlyIleLeuLeuTyrGluThrPhe 684
Dy 1294 AACAGTTCTCCATCAAGTCCGAGCTCTGGGCAATTTGGAGTATTGCTTTGGGAAATTGCT 1353
Qy 685 SerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnThrArgGluPheValGlu 704
Dy 1354 ACCTATGGCATGTCCCTTACCCGGGAATTTGACCGTTCCTCCAGGTTGTATGAGCTGTAGAG 1413
Qy 705 LysGlyGlyArgLeuProCysProGluLeuCysProAspAlaValPheArgLeuMetGlu 724
Dy 1414 AAGGACTACCGCATGAAGCGCCAGAGGTCGCCAGAGAGGTCTATGAACCTATGCGGA 1473
Qy 725 GlnCysTrpAlaTyrGluProGlyGlnArgProSerPheSerThrIleTyrGlnGluLeu 744
Dy 1474 GCATGTTGGCAGTGGAAATCCCTCTGACCGGCGCTCTTGTGTAATCCACCAAGCCTTT 1533
Qy 745 GlnSerile 747
Dy 1534 GAAACAATG 1542

RESULT 13
US-10-439-703-5
; Sequence 5, Application US/10439703
; Publication No. US20040018527A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Jenny
; APPLICANT: O'Connell, Peter
; TITLE OF INVENTION: Differential Patterns of Gene Expression that Predict for Docetax
```

Wed Aug 10 16:17:25 2005

Db 1427 GAGAGAAAAA... 1486
Qy 625 AsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAlaAspGlyValTyrAla 644
Db 1487 CACTGGTGAAGTAGCTGATTTTGGCTGAGCAGAGTTGATGACACGGGACACCTACACA 1546
Qy 645 AlaSerGlyGlyLeuArgGlnValProValIleThrAlaProGluAlaLeuAsnTyr 664
Db 1547 GCCCATGCTGGAGCCAAG---TTCCCCATCAATGGACTGCACCCGAGAGCCTGGCCTAC 1603
Qy 665 GlyArgTyrSerSerGluSerAspValTyrPheGlyIleLeuLeuTyrGluThrPhe 684
Db 1604 AACAAAGTTCTCCATCAAGTCCGAGCTCTGGGCATTTGGAGTATTGCTTTGGGAAATTGCT 1663
Qy 685 SerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThrArgGluPheValGlu 704
Db 1664 ACCTATGGCATGTCCCTTACCCGGGAATTGACCGTTCCCGAGGTGTATGAGCTGCTAGAG 1723
Qy 705 LysGlyGlyArgLeuProCysProGluLeuCysProAspAlaValPheArgLeuMetGlu 724
Db 1724 AAGGACTACCGCATGAAGCGCCAGAGAGGCTGCCAGAGAGGTCTATGAACCTCATGCGA 1783
Qy 725 GlnCysTrpAlaTyrGluProGlyGlnArgProSerPheSerThrIleTyrGlnGluLeu 744
Db 1784 GCATGTGGCAGTGGAAATCCCTCTGACCGGGCCCTCTTGTGTAATCCACCAAGCCTTT 1843
Qy 745 GlnSerIle 747
Db 1844 GAAACAATG 1852
RESULT 14
US-10-457-954-5
; Sequence 5, Application US/10457954
; Publication No. US20040005623A1
; GENERAL INFORMATION:
; APPLICANT: Longley, B. Jack
; TITLE OF INVENTION: Method of determining tumor sensitivities to therapeutic drugs
; FILE REFERENCE: 960296.98890
; CURRENT APPLICATION NUMBER: US/10/457,954
; CURRENT FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/387,370
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/387,406
; PRIOR FILING DATE: 2002-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 3450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3447)
; FEATURE:
; NAME/KEY: misc structure
; LOCATION: (730)..(765)
; OTHER INFORMATION: encode
; OTHER INFORMATION: pocket
; FEATURE:
; NAME/KEY: misc structure
; LOCATION: (931)..(1077)
; OTHER INFORMATION: encode
; OTHER INFORMATION: pocket
; FEATURE:
; NAME/KEY: misc structure
; LOCATION: (1141)..(1206)
; OTHER INFORMATION: encode
; OTHER INFORMATION: activation loop
US-10-457-954-5
Alignment Scores: 1.89e-48 Length: 3450
Pred. No.:

; TITLE OF INVENTION: Chemosensitivity and Chemoresistance
; FILE REFERENCE: HO-P2482US1/10205813
; CURRENT APPLICATION NUMBER: US/10/439,703
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/381,141
; PRIOR FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5744
; TYPE: DNA
; ORGANISM: Human
US-10-439-703-5
Alignment Scores: 2.79e-48 Length: 5744
Pred. No.: 138 Matches: 1348
Score: 624.50
Percent Similarity: 53.79% Conservative: 68
Best Local Similarity: 36.03% Mismatches: 128
Query Match: 16.10% Indels: 49
Gaps: 10
DB: 17
US-10-660-763-2 (1-752) x US-10-439-703-5 (1-5744)
Qy 405 AspArgHisSerThrSerSerGluGlnGluArgGlyGlyArgThrProThrLeu 424
Db 731 GAGAACATCTCTGGTACCATGGGCTGTGTCGCCAATGCCGCTGAGTATCCG----- 784
Qy 425 GluIleLeuLysSerHisIleSerGlyIlePheArgProLysPheSer----- 440
Db 785 -----CTGAGCAGCGGGATCAATGCCAGCTTCTTGTGGCTGAGAGTGAGAGTCCT 838
Qy 440 ----- 440
Db 839 AGCCAGGTCCATCTCGCTGAGATACGAAGGAGGTTACCATTTACAGATCAACACT 898
Qy 441 -----AsnLeuArgLeuGluGlyGlyPheProSerIleProLeuLeu 456
Db 899 GCTTCTGATGGCAAGCTCTACGTCTCTCCGAGAGCGGCTTCAACACCTGGCGAGTTG 958
Qy 457 IleAspHis-----LeuLeuSerThr-----GlnGlnProLeuThr 468
Db 959 GTTCATCATCTTCAACGGTGGCGAGCGGCTCATCCACCGCTCATATTATCCAGCCCA 1018
Qy 469 LysLysSerGlyValValLeuHisArgAlaValProLys---AspLysTrpValLeuAsn 487
Db 1019 AAGCGCAACAAGCCCACTGCTATGTGTGTCTCCCACTACGACAAGTGGGAGATGGA 1078
Qy 488 HisGluAspLeuValLeuGlyGluGlnIleGlyArgGlyAsnPheGlyGluValPheSer 507
Db 1079 CGCAGGACATCACCATGACGACCAAGCTGGGGGGCCAGTACGGGGAGGTGTACGAG 1138
Qy 508 GlyArgLeuArgAlaAspAsnThrLeuValAlaValLysSerCysArgGlu---ThrLeu 526
Db 1139 GCGGTGTGAAGAAATACAGCTGACGGTGGCGGTGAGACCTTGAAGAGGAGGACACCATG 1198
Qy 527 ProProAspLeuLysAlaLysPheLeuGlnGluAlaArgIleLeuLysGlnTyrSerHis 546
Db 1199 GAGGTGAA-----GAGTCTTGAAGAAGTGCAGTCAATGAAGAGATCAACAC 1249
Qy 547 ProAsnIleValArgLeuIleGlyValCysThrGlnLysGlnProIleTyrIleValMet 566
Db 1250 CCTAACCTAGTGCAGTCTCTGGGGTCTGCACCCGGGAGCCCGCTTCTATATCATCACT 1309
Qy 567 GluLeuValGlnGlyArgPheLeuThrPheLeuArgThrGluGlyAlaArgLeuArg 586
Db 1310 GAGTTCAIGACCTACGGGACCTCTTGGACTACCTGAGG---GAGTGCACCGGAGGAG 1366
Qy 587 ValLys-----ThrLeuLeuGlnMetValGlyAspAlaAlaGlyMetGluTyrLeu 604
Db 1367 GTGAACGCGGTGCTGCTGTACATGGCCACTCAGTCTCGTCAAGCCATGAGTACCTA 1426
Qy 605 GluSerLysCysCysIleHisArgAspLeuAlaAlaArgAsnCysLeuValThrGluLys 624

Score: 623.00 Matches: 158
Percent Similarity: 48.21% Conservative: 84
Best Local Similarity: 31.47% Mismatches: 150
Query Match: 16.06% Indels: 110
DB: 17 Gaps: 17

US-10-660-763-2 (1-752) x US-10-457-954-5 (1-3450)

QY	341	GlulGluAenThrHisProArgGluArgValGlnLeuLeuGlyLysArgGlnValLeu	360
DB	85	AAGGAATCATCGAGCATCGGGGTCCACACTCAATGTTTGTGGAACATGAGCCCTT	144
QY	361	GlnGluALeu-----GlnGlyLeuGlnValAlaLeuCysSerGln	374
DB	145	CAGCGCCAGTAGACTCTGACTTTGAGCCTCAGGGTCTGAGTGAAGCC-----	192
QY	375	AlaLysLeuGlnAlaGlnGlnGluLeuLeuGlnThrLysLeuGluHisLeuGlyProGly	394
DB	193	GCTCGTTGAACCTCCAGGAAGAACCTTCTC-----GCTGGACCCAGT	234
QY	395	GluProProValLeuLeuLeuGln-----AspAsp---	405
DB	235	GAAATGACCCCAACCTTTCTGTGCACTGATGATTTTGTGGCCAGTGGAGATAACACT	294
QY	406	-----ArgHisSerThrSerSer	411
DB	295	CTAAGCATAACTAAAGGTGAAAGCTCCGGGTCTTAGGCTATAATCAACAATGGGAAATG	354
QY	412	SerGluGlnGluArgGluGlyGlyArg-----ThrPro---	422
DB	355	TGTGAAGCCCAACCAAAATGCGCAAGGCTGGTCCCAAGCAACTACATCACGCCAGTC	414
QY	423	---ThrLeuGlu-----	425
DB	415	AACAGTCTGGAGAAACACTCTCTGGTACCATGGCCCTGTGTCCCGCAATGCCGCTGAGTAT	474
QY	426	IleLeuLysSerHisIleSerGlyIlePheArgProLysPheSer-----	440
DB	475	CTGCTGAGCAGCGGGATCAATGCGAGCTTCTTGGTGGCGTGGAGAGTGAGAGCGCTCTGGC	534
QY	440	-----	440
DB	535	CAGAGTCCATCTCGCTGAGATACGAAGGGAGGGTGTACCAATTACAGATCAACACTGCT	594
QY	441	-----AsnLeuTyrrArgLeuGluGlyGluGlyPheProSerIleProLeuLeuIle	457
DB	595	TCTGATGGCAAGCTCTACGTCTCTCCGAGAGCCGCTTCAACACCCTCGCGAGTTGTT	654
QY	458	AspHis-----LeuLeuSerThr-----GlnGlnProLeuThrLys	469
DB	655	CATCATCATTCACGGTGGCCGAGGGGCTCATCACACGCTCCATTATCCAGCCCAAG	714
QY	470	LysSerGlyValValLeuHisArgAlaValProLys-----AspLysTrpValLeuAsnHis	488
DB	715	CGCAACAGCCCACTGCTCTATGGTGTGTGTCCTCCCAACTACGACAGTGGGAGATGGAACGC	774
QY	489	GluAspLeuValLeuGlyGluGlnIleGlyArgGlyAsnPheGlyGluValPheSerGly	508
DB	775	ACGATATCCATGAGACACAGCTGGCGGGGGCCAGTACCGGGAGGTGTACAGGGC	834
QY	509	ArgLeuArgAlaAspAsnThrLeuValAlaValLysSerCysArgGlu---ThrLeuPro	527
DB	835	GTGTGGAAGAAATACAGCTGACGTGGCGGTGAGAGACCTTGAAGGAGGACACCATGAG	894
QY	528	ProAspLeuLysAlaLysPheLeuGlnGlnAlaAlaArgLysLeuGlyThrSerHisPro	547
DB	895	GTGGAA-----GAGTCTTTGAAGAAGCTGTCAGTGCATGAAAGAGATCAACACCCCT	945
QY	548	AsnIleValArgIleGlyValCysThrGlnLysGlnProIleTyrrIleValMetGlu	567
DB	946	AACCTGGTCAGCTCTCTGGGTGTGACCCCGGGAGCCCGCTTCTATATCATCACTGAG	1005
QY	568	LeuValcInGlyAspPheLeuThrPheLeuArgThrGluGlyAlaArgLeuArgVal	587

US-10-263-480-1

Sequence 1, Application US/10263480
Publication No. US20030170851A1
GENERAL INFORMATION:
APPLICANT: No. US20030170851A1artis AG
TITLE OF INVENTION: Organic Compounds
FILE REFERENCE: Case 4-32175PI/PROV
CURRENT APPLICATION NUMBER: US/10/263,480
CURRENT FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 3393
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(3393)
US-10-263-480-1

Alignment Scores:
Pred. No.: 2,296-48 Length: 3393
Score: 622.00 Matches: 158
Percent Similarity: 48.67% Conservative: 79
Best Local Similarity: 32.44% Mismatches: 136
Query Match: 16.04% Indels: 114
DB: 17 Gaps: 17

US-10-660-763-2 (1-752) x US-10-263-480-1 (1-3393)

QY	360	LeuGlnGluAlaLeu-----GlnGlyLeuGlnVal	369
DB	73	CTGGGAAGAGCCCTTCAGCGGCAGCTAGCATCTGACTTTGAGCCTCAGGGTCTGAGTGAA	132

Wed Aug 10 16:17:25 2005

641 GlyValTyrAlaAlaSerGlyLeuArgGlnValProValIleThrPheGlu 660
 1171 GACACCTACACAGCCCATGCTGGAGCCAG--TTCCCCATCAATGGACTGCACCCGAG 1227
 661 AlaLeuAsnTyrGlyArgTyrSerSerGluSerAspValTyrPheGlyIleLeuLeu 680
 1228 AGCCTGGCCTACAAAGTTCTCCATCAAGTCCGAGCTCTGGGCACTTTGGAGTATTGCTT 1287
 681 TrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnThrArg 700
 1288 TGGGAAATTGTCTACCTATGGCATGTCCCTTACCCGGGAATTGACCTGTCCAGGTGTAT 1347
 701 GluPheValGluLeuGlyArgLeuProCysProGluLeuCysProAspAlaValPhe 720
 1348 GAGCTGCTAGAGAAGGACTACCGCATGGAGCGCCGAGAGGCTCCCGAGAGGTCTAT 1407
 721 ArgLeuMetGluGlnCysTrpAlaTyrGluProGlyGlnArgProSerPheSerThrIle 740
 1408 GAACTCATCGGAGCATGTTGGCAGTGGAAATCCCTCTGACCGCGCTCTCTTGTGTAATC 1467
 741 TyrGlnGluLeuGlnSerIle 747
 1468 CACCAAGCCTTTGAAACAATG 1488

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 Job time : 1701 secs

370 AlaLeuCysSerGlnAlaIleLeuGlnAlaGlnGlnLeuLeuGlnThrIleLeuGlu 389
 133 GCC-----GCTGTTGGAACTCCAGGAACCTTCTC----- 165
 390 HisLeuGlyProGlyGluProProValLeuLeuGln----- 403
 166 ---GCTGGACCCAGTGAATAATGACCCACCTTTTCTGTCACCTGATGATTTGTGGCC 222
 404 ---AspAsp----- 406
 223 AGTGGAGATAACACTTAAGCATAACTAAAGCTGAAAGCTCCGGTCTTAGGCTATAAT 282
 420 ----- 420
 407 HisSerThrSerSerGluGlnArgGluGlyArg----- 420
 283 CACAATGGGNAATGGTGAAGCCCAACCAAAATGGCCAGGTGGGTGCCAAGCAAC 342
 421 -----ThrLeuGlu----- 425
 343 TACATCAGCCGAGTCAACAGCTCTGGAGAAACACTCTCTGGTACCATGGGCTGTCTCCGC 402
 426 -----IleLeuLeuSerHisIleSerGlyIlePheArgProIlePheSer 440
 403 AATGCCGCTGAGTATCTGCTGAGCAGCGGATCAATGGCAGCTTCTTGGTGGTGNAGT 462
 440 ----- 440
 463 GAGAGCAGTCTGGCCAGAGTCCATCTCGTGAGATACGAAGGAGGTGTACCATTAC 522
 441 -----AsnLeuTyrArgLeuGluGlyGluGlyPheProSer 452
 523 AGGATCAACACTCTCTGATGGCAAGCTCTACGTCTCTCCGAGAGCCGCTTCAACACC 582
 453 IleProLeuLeuIleAspHis-----LeuLeuSerThr---Gln 464
 583 CTGGCCGAGTGGTTCATCATCATCAACGGTGGCGGCTCATCCACCGCTCCAT 642
 465 GlnProLeuThrIleLeuSerGlyValValLeuHisArgAlaValProIle---AspLys 483
 643 TATCCAGCCCAAGCGCAACAGCCACTGCTATGTGTGTCTCCCACTAGCAACAG 702
 484 TrpValLeuAsnHisGluAspLeuValLeuGlyGluGlnIleGlyArgGlyAsnPheGly 503
 703 TGGGAGATGGAACGACGAGCATCACATGAGCAACAGCTGGCGGGGCGCAGTACGGG 762
 504 GluValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaValIleSerCysArg 523
 763 GAGGTGTACGAGGCGGTGTGAAGAAATACAGCTGACCGTGGCGGTGAAGACCTTGAAG 822
 524 Glu---ThrLeuProProAspLeuLeuAlaIlePheLeuGlnGluAlaArgIleLeuLys 542
 823 GAGGACACCATGGAGGTGGA-----GAGTCTTGAAGAAAGCTGCAGTCAATGAA 873
 543 GlnTyrSerHisProAsnIleValArgLeuIleGlyValCysThrGlnLysGlnProIle 562
 874 GAGATCAACACCTTAACCTGTCAGCTCTCTGGGTCTGCACCGCGGAGCCCGCTTC 933
 563 TyrIleValMetGluLeuValGlnGlyArgPheLeuThrPheLeuArgThrGluGly 582
 934 TATATCATCATGAGTTCATGACCTACCGGAACTCTCTGGAGCTACCTGAGG---GAGTGC 990
 583 AlaArgLeuArgValLys-----ThrLeuLeuGlnMetValGlyAspAlaAlaGly 600
 991 AACCGGAGGAGGTGAACCGCTGTGTCTGTATGTCGACCTCAGATCTGTCAGCC 1050
 601 MetGluTyrLeuGlnSerLysCysIleHisArgAspLeuAlaAlaArgAsnCysLeu 620
 1051 ATGGAGTACCTGAGAGAAACCTTCATCCACAGATCTTGTCTGCCGAACTGCTG 1110
 621 ValThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluAlaAsp 640
 1111 GTAGGGAGAACCACTTGGTGAAGTAGTATTTTGGCCTGAGCAGGTGTGATGACAGG 1170

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Deiop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2137	55.1	15297	3	US-09-817-180-3
4	2137	55.1	15297	4	US-10-003-295-3
5	624.5	16.1	3623	1	US-08-306-691B-35
6	624.5	16.1	5434	4	US-09-949-016-527
7	622	16.0	5763	4	US-09-949-016-3759
8	607.5	15.7	1521	2	US-08-604-989A-10
9	607.5	15.7	1713	3	US-09-741-154-1
10	605.5	15.6	1942	2	US-08-604-989A-11
11	605.5	15.6	2000	3	US-08-426-509A-1
12	605.5	15.6	2000	4	US-08-232-545-1

13	605.5	15.6	2000	5	PCT-US95-05008-1	Sequence 1, Appli
14	602	15.5	1398	2	US-08-604-989A-9	Sequence 9, Appli
15	598.5	15.4	2572	4	US-09-949-016-5357	Sequence 5357, Ap
16	598	15.4	2574	3	US-09-142-529-2	Sequence 2, Appli
17	598	15.4	2574	4	US-10-045-428A-2	Sequence 2, Appli
18	597	15.4	3650	4	US-09-949-016-454	Sequence 454, App
19	596.5	15.4	3622	4	US-09-949-016-5518	Sequence 5518, Ap
20	596.5	15.4	3663	4	US-09-919-172-84	Sequence 84, Appl
21	593	15.3	1994	4	US-09-949-016-1967	Sequence 1967, Ap
22	591	15.2	2456	4	US-09-016-434-1476	Sequence 1476, Ap
23	591	15.2	2500	3	US-08-426-509A-3	Sequence 3, Appli
24	591	15.2	2500	4	US-08-232-545-3	Sequence 3, Appli
25	591	15.2	2500	5	PCT-US95-05008-3	Sequence 3, Appli
26	585.5	15.1	6381	4	US-09-949-016-755	Sequence 755, App
27	582.5	15.0	2505	1	US-08-391-615-1	Sequence 1, Appli
28	581.5	15.0	2440	1	US-08-160-861-2	Sequence 2, Appli
29	581.5	15.0	2442	1	US-08-542-363-3	Sequence 3, Appli
30	581.5	15.0	2442	3	US-09-100-089-3	Sequence 3, Appli
31	581.5	15.0	2442	3	US-09-670-827-3	Sequence 3, Appli
32	581.5	15.0	2442	4	US-09-827-949-3	Sequence 3, Appli
33	574.5	14.8	1467	4	US-09-579-182-2	Sequence 2, Appli
34	574.5	14.8	1548	3	US-09-099-053-1	Sequence 1, Appli
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36	573.5	14.8	2608	1	US-08-160-861-1	Sequence 1, Appli
37	573.5	14.8	6226	1	US-08-542-363-1	Sequence 1, Appli
38	573.5	14.8	6226	3	US-09-100-089-1	Sequence 1, Appli
39	573.5	14.8	6226	3	US-09-670-827-1	Sequence 1, Appli
40	573.5	14.8	6226	4	US-09-827-949-1	Sequence 1, Appli
41	573	14.8	3791	3	US-09-377-310-1	Sequence 1, Appli
42	571.5	14.7	4975	2	US-08-249-687C-1	Sequence 1, Appli
43	571.5	14.7	4989	2	US-08-666-392A-3	Sequence 3, Appli
44	571.5	14.7	4989	2	US-08-625-819-1	Sequence 1, Appli
45	571.5	14.7	4989	3	US-08-755-558-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-817-180-1
; Sequence 1, Application US/09817180
; Patent No. 6340584
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183
; CURRENT APPLICATION NUMBER: US/09/817,180
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2674
; TYPE: DNA
; ORGANISM: Human
; US-09-817-180-1

Alignment Scores:

Pred. No.: 0
Score: 3879.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 3
Length: 2674
Matches: 752
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-660-763-2 (1-752) x US-09-817-180-1 (1-2674)

Qy	1	MetGlyPheSerSerGluLeuCySerProGlnGlyHisGlyValLeuGlnMetGln	20
Db	72	ATGGGCTCTCTCTCTGAGCTGTGCAGCCCGGCGCACCGGGTCTCTGCAGCAATGCAG	131
Qy	21	GLUAlaGluLeuArgLeuLeuGluGlyMetArgLysTrpMetAlaGlnArgValLysSer	40

Db	132	GAGGCGAGCTTCGTCTACTGAGGGGCATGAGAAAGTGCATGGCCACGCGGTCAAGAGT	191	Qy	401	LeuLeuGlnAspAspArgHisSerThrSerSerSerGluGlnGluArgGluGlyArg	420
Qy	41	AspArgGluTyrAlaGlyLeuLeuHisHisMetSerLeuGlnAspSerGlyGlyGlnSer	60	Db	1272	CTCTCGCAGGATGACCGCCACTCCACGCTCGTCTCGAGCAGGAGCGAGAGGGGGAGG	1331
Db	192	GACAGGGAGTATCAGGAGCTGCTTACCACATGTCCCTGCAGGACAGTGGGGGCAGAGC	251	Qy	421	ThrProThrLeuGluLeuLeuLysSerHisIleSerGlyIlePheArgProLysPheSer	440
Qy	61	ArgAlaIleSerProAspSerProIleSerGlnSerTrpAlaGluIleThrSerGlnThr	80	Db	1332	ACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCGGCCCCCAAGTCTCG	1391
Db	252	CGGGCCATCAGCCCTGACAGCCCATCAGTCACTGCTGGCTGAGATCACCAGGCCAACT	311	Qy	441	AsnLeuTyrArgLeuGluGlyGluGlyPheProSerIleProLeuLeuIleAspHisLeu	460
Db	81	GluGlyLeuSerArgLeuLeuArgGlnHisAlaGluAspLeuAsnSerGlyProLeuSer	100	Db	1392	AACCTGTACCGACTGGAAGGGGAAGGCTTTCTAGCATCTCTTTGCTCATCGACCACTA	1451
Qy	312	GAGGCGCTGAGCGCTTGTCTGGCCAGCAGCAGAGGATCTGAATCTAGGGCCCCCTGAGC	371	Qy	461	LeuSerThrGlnGlnProLeuThrTyrLysSerGlyValValLeuLeuHisArgAlaValPro	480
Db	101	LysLeuSerLeuLeuIleArgGluArgGlnGlnLeuArgLysThrTyrSerGluGlnTrp	120	Db	1452	CTGGACCCACGACGCCCCCTCACAAAGAAGAGTGGTGTGTCTGCACAGGGCTGTGCC	1511
Db	372	AAGCTGAGCTGTCTCATCTCCGGGAACGGCAGCAGCTTCGCAAGACCTACAGCGAGCAGTGG	431	Qy	481	LysAspLysTrpValLeuAsnHisGluAspLeuValLeuGlyGluGlnIleGlyArgGly	500
Qy	121	GlnGlnLeuGlnGlnLeuThrLysThrHisSerGlnAspIleGluLysLeuLysSer	140	Db	1512	AAGGACAAAGTGGGTGCTGAACCATGAGGACCTGGTGTGGTGGAGCAGATTGGACGGGG	1571
Db	432	CAGCAGCTGCAGCAGGAGCTCACCAAGACCACAGCCAGGACATTTGAGAAGCTGAAGAGC	491	Qy	501	AsnPheGlyGluValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaValLys	520
Qy	141	GlnTyrArgAlaLeuAlaArgAspSerAlaGlnAlaLysArgLysTyrGlnGluAlaSer	160	Db	1572	AACCTTGGCGAAGTGTTCAGCGGACGCTCGAGCGCCCTCGAGCCGACCAACACCTGTGGCGGTGAAG	1631
Db	492	CAGTACCAGCTCTGGCAGCGGACAGTGCCTCCAGCCAGCCAGCTACCCAGGAGGCCAGC	551	Qy	521	SerCysArgGluThrLeuProAspLeuLysAlaLysPheLeuGlnGluAlaArgIle	540
Qy	161	LysAspLysAspArgAspLysAlaLysAspLysTyrValArgSerLeuTrpLysLeuPhe	180	Db	1632	TCTTGTGAGAGACGCTCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGGATC	1691
Db	552	AAAGACAGGACCTGCACAGGCCACAGGACAAGTATGTGGCAGCGCTGTGGAAGCTCTTT	611	Qy	541	LeuLysGlnTyrSerHisProAsnIleValArgLeuIleGlyValCysThrGlnLysGln	560
Qy	181	AlaHisHisAsnArgTyrValLeuGlyValArgAlaAlaGlnLeuHisHisGlnHis	200	Db	1692	CTGAAGCAGATACAGCCACCCCAACATCGTGGTCTCATTTGGTGTCTGCACCCAGAGCAG	1751
Db	612	GCTACCAACAACCGCTATGTCTGGGGCTGGGGCTGCGGAGTACACACAGCAGCCAC	671	Qy	561	ProIleTyrIleValMetGluLeuValGlnGlyClyAspPheLeuThrPheLeuArgThr	580
Qy	201	HisGlnLeuLeuLeuProGlyLeuLeuArgSerLeuGlnAspLeuHisGluGluMetAla	220	Db	1752	CCCATCTACATCGTCATGGAGCTTGTGCGGGGGCGACCTTCTCTGAGACTTCTCTCCGACG	1811
Db	672	CACCAAGCTCTGCTGCCCGGGCTGCTGGGTCACTGCAGGACCTGCAGCAGGAGATGGCT	731	Qy	581	GluGlyAlaArgLeuArgValLysThrLeuLeuGlnMetValGlyAspAlaAlaAlaGly	600
Qy	221	CysIleLeuLysGluIleLeuGlnGluTyrLeuGluIleSerSerLeuLeuGlnAspGlu	240	Db	1812	GAGGGGGCCCGCTCGGGTGNAGACTCTGCTGCAGATGGTGGGGATGCAAGCTGTGCTGC	1871
Db	732	TGCATCTCGAAGGAGATCTCGCAGGAATACCTGGAGATTAGACGCTTGTGCAGGATGAG	791	Qy	601	MetGluTyrLeuGluSerLysCysIleHisArgAspLeuAlaAlaArgAsnCysLeu	620
Qy	241	ValValAlaIleHisArgGluMetAlaAlaAlaAlaArgIleGlnProGluAlaGlu	260	Db	1872	ATGGAGTACTCGAGAGCAAGTGTGTCATCCACGGGACCTGGGCTCTCGGAACCTGCTCG	1931
Db	792	GTGGTGGCCATTACCGGAGATGCTGCAGCTGTGCTGCCCATCCAGCCTGAGGCTGAG	851	Qy	621	ValThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAlaAsp	640
Qy	261	TyrGlnGlyPheLeuArgGlnTyrGlySerAlaProAspValProProCysValThrPhe	280	Db	1932	GTGACAGAGAAGAAATGTCTCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGAGCCGAT	1991
Db	852	TACCAAGGCTTCTCGCAGCAGTATGGGTCCGCACCTGCAGCTCCACCTGTGTCACTTC	911	Qy	641	GlyValTyrAlaAlaSerGlyGlyLeuArgGlnValProValLysTrpThrAlaProGlu	660
Qy	281	AspGluSerLeuLeuGluGlyGluProLeuGluProGlyGluLeuGlnLeuAsnGlu	300	Db	1992	GGGGTCTATGACGCTTCAGGGGGCCTCAGACAAAGTCCCGGTGAAGTGAACCCACCTGAG	2051
Db	912	GATGAGTCACTGTCTGAGGAGGTGAAACCGCTGGAGCCTGGGGCTCCAGCTGAACGAG	971	Qy	661	AlaLeuAsnTyrClyArgTyrSerSerGluSerAspValTrpSerPheGlyIleLeuLeu	680
Qy	301	LeuThrValGluSerValGlnHisThrLeuThrSerValThrAspGluLeuAlaValAla	320	Db	2052	GCCCTTTAACTACCGCCGCTACTCTCCGAAAGGGACGTGTGGAGCTTTGGCATCTTGCTC	2111
Db	972	CTGACTGTGAGAGCGTGCAGCACACGCTGACCTCAGTCAGATGAGTGTGCTGTGGCC	1031	Qy	681	TrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThrArg	700
Qy	321	ThrGluMetValPheArgArgGlnGluMetValThrGlnLeuGlnGlnLeuLeuArgAsn	340	Db	2112	TGGGAGNACCTTCAGCTGGGGGCTCCCTCATCCCAACCTCAGCAATCAGCAGACCGG	2171
Db	1032	ACCGAGATGGTGTTCAGCGCGCAGGAGATGGTTACGACAGTGCACAGGAGCTCCGGAAT	1091	Qy	701	GluPheValGluLysGlyArgLeuProCysProGluLeuCysProAspAlaValPhe	720
Qy	341	GluGluGluAsnThrHisProArgGluArgValGlnLeuLeuGlyLysArgGlnValLeu	360	Db	2172	GAGTTTGTGAGAAGGGGGGCGCTGTGCCCTTGCCCAAGAGCTGTCTCTGATGCCGTGTC	2231
Db	1092	GAAAGGAGAACACCCACCCCGGAGCGGCTGCAGCTGTGGGCAAGGCAAGTGTG	1151	Qy	721	ArgLeuMetGluGlnCysTrpAlaTyrGluProGlyGlnArgProSerPheSerThrIle	740
Qy	361	GlnGluAlaLeuGlnGlyLeuGlnValAlaLeuCysSerGlnAlaLysLeuGlnAlaGln	380	Db	2232	AGGCTCATGGAGCAGTGTCTGGGCTATGAGCTGGGCGAGCGGCCAGCTTTCAGACCATC	2291
Db	1152	CAAGAAGCACTGCGAGGGGCTGACAGTGGCTGTGACGACCGCCCAAGCTGCGAGCC	1211	Qy	741	TyrGlnGluLeuGlnSerIleArgLysArgHisArg	752
Qy	381	GlnGluLeuLeuGlnThrLysLeuGluHisLeuGlyProGlyGluProProValLeu	400	Db	2292	TACGAGGAGCTGCAGACATCCGAAAGCGGCACTCGG	2327
Db	1212	CAGGAGTTGCTGCAGACCAAGCTGGAGCACCTGGGGCCCGCGAGGCCCGCTGTGCTG	1271				

RESULT 2

US-10-003-295-1
; Sequence 1, Application US/10003295
; Patent No. 6686187
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIV
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-003-295-1

Alignment Scores:
Pred. No.: 0 Length: 2674
Score: 3879.00 Matches: 752
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-660-763-2 (1-752) x US-10-003-295-1 (1-2674)

QY	1	MetGlyPheSerSerGluLeuCysSerProGlnGlyHisGlyValLeuGlnGlnMetGln	20
DB	72	ATGGGCTTCTCTTCTGAGCTGTGCAGGCCCCAGGGCCACGGGGTCTTGCACGAATGCAG	131
QY	21	GluAlaGluLeuArgLeuGluGlyMetArgIysTrpMetAlaGlnArgValIysSer	40
DB	132	GAGGCCAGGCTTCTCTACTGGAGGGCATGAGAAGTGGATGGCCACGGGTCAGAGT	191
QY	41	AspArgGluTyrAlaGlyLeuLeuHisMetSerLeuGlnAspSerGlyGlnSer	60
DB	192	GACAGGAGATGTCAGGACTGCTTCCACCATGTCCTGCAGGACAGTGGGGCCAGAGC	251
QY	61	ArgAlaIleSerProAspSerProIleSerGlnSerTrpAlaGluIleThrSerGlnThr	80
DB	252	CGGGCCATCAGCCCTGACGCCCATCAGTCAGTCTCTGGGCTGAGATCACCAGCCAACT	311
QY	81	GluGlyLeuSerArgLeuLeuArgGlnHisAlaGluAspLeuAsnSerGlyProLeuSer	100
DB	312	GAGGGCTTGAGCCCTTGCTGCGGCACAGCAGAGGATCTGAAGTCTGAGGCCCTGAGC	371
QY	101	LysLeuSerLeuLeuIleArgGluArgGlnGlnLeuArgIysTrpTyrSerGluGlnTrp	120
DB	372	AAGCTGAGCCTTGCTCATCCGGAAACGGCAGCAGCTTCGAAGACCTACAGGAGCAGTGG	431
QY	121	GlnGlnLeuGlnGlnGluLeuThrLysThrHisSerGlnAspIleGluLysLeuLysSer	140
DB	432	CAGCAGCTGCAGCAGGAGCTCACCAGACCCACAGCCAGGACATTCGAAGCTGAAGAGC	491
QY	141	GlnTyrArgAlaLeuAlaArgAspSerAlaGlnAlaLysArgLysTyrGlnGluAlaSer	160
DB	492	CAGTACCGAGCTCTGGCAGCGGACAGTGCCCAAGCCCAAGCGCAAGTACAGGAGGCCAGC	551
QY	161	LysAspLysAspArgAspLysAlaLysAspLysTyrValArgSerLeuTyrLysLeuPhe	180
DB	552	AAAGACAAGGACCGTGACAGGCCAAGGACAAAGTATGTGGCAGCCTGTGGAAGCTCTTT	611
QY	181	AlaHisHisAsnArgTyrValLeuGlyValArgAlaAlaGlnLeuHisGlnHisHis	200
DB	612	GCTCACCACACCCGCTATGTCTGGGGCTGGGGCTGGCGAGCTACACCAACAGCACCAC	671
QY	201	HisGlnLeuLeuLeuProGlyLeuLeuArgSerLeuGlnAspLeuHisGluGluMetAla	220
DB	672	CACCAGCTCTCTGCTGCCCCGGCTCTGCTGGGTCACTGCAGGACCTTGCACGAGGAGATGGCT	731

QY	221	CysIleLeuLysGluIleLeuGlnGluTyrLeuGluLysSerSerLeuValGlnAspGlu	240
DB	732	TGCATCTCTGAAGGAGATCTCTGCAGGAATACCTGAGATTAGCAGCCTGGTGCAGGATGAG	791
QY	241	ValValAlaIleHisArgGluMetAlaAlaAlaAlaArgIleGlnProGluAlaGlu	260
DB	792	GTGGTGGCCATTCCACCGGAGATGGCTGCAGCTGCTGCCCGCATCCAGCCTTGAGGCTGAG	851
QY	261	TyrGlnGlyPheLeuArgGlnTyrGlySerAlaProAspValProProCysValThrPhe	280
DB	852	TACCAAGGCTTCTGCGACAGATGGTCCGCACCTGACGTCCACCCCTGTGTCACTGTC	911
QY	281	AspGluSerLeuLeuGluGlyGlyProLeuGluProGlyGluLeuGlnLeuAsnGlu	300
DB	912	GATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGCTGGGAGCTCCAGCTGAACGAG	971
QY	301	LeuThrValGluSerValGlnHisThrLeuThrSerValThrAspGluLeuAlaValAla	320
DB	972	CTGACTGTGGAGAGCGTGCAGCACAGCTGACCTCAGTGCAGATGAGCTGGCTGTGGCC	1031
QY	321	ThrGluMetValPheArgArgGlnGluMetValThrGlnLeuGlnGlnLeuArgAsn	340
DB	1032	ACCGAGATGCTGTTTCAGCGCGCAGGAGATGTTTACGCAGCTGCCAACAGGAGCTCCGGAT	1091
QY	341	GluGluGluAsnThrHisProArgGluArgValGlnLeuLeuGlyLysArgGlnValLeu	360
DB	1092	GAAGAGGAGAAACACCCACCCCGGAGCGGTGCAGCTGCTGGGCAAGAGCAAGTGTCTG	1151
QY	361	GlnGluAlaLeuGlnGlyLeuGlnValAlaLeuCysSerGlnAlaLysLeuGlnAlaGln	380
DB	1152	CAAGAGACACTGCGGGGCTGTCAGGTAGCGCTGTGCAGCGCAGGCAAGCTGCAGGCCAG	1211
QY	381	GlnGluLeuLeuGlnThrLysLeuGluHisLeuGlyProGlyGluProProValLeu	400
DB	1212	CAGGAGTGTGTCAGACCAAGCTGGAGCACTGGGCCCCCGCGAGCCCCGCCCTGTGCTG	1271
QY	401	LeuLeuGlnAspAspArgHisSerThrSerSerSerGluGlnGluArgGluGlyArg	420
DB	1272	CTCTTGAGGATGACGCCACTCAGCTGCTCTCGGAGCAGGAGCGAGGGGGGAGG	1331
QY	421	ThrProThrLeuGluIleLeuLysSerHisIleSerGlyIlePheArgProLysPheSer	440
DB	1332	ACACCCACGCTGGAGATCTCTTAAGAGCCACATCTCAGGAATCTTCCGCCCCCAAGTCTCG	1391
QY	441	AsnLeuTyrArgLeuGluGlyGluGlyPheProSerIleProLeuLeuIleAspHisLeu	460
DB	1392	AACTGTACCGACTGGNAGGGGAAGGCTTCTCTAGCATTCCTTTGCTCATCGACCACCTA	1451
QY	461	LeuSerThrGlnGlnProLeuThrLysLysSerGlyValValLeuHisArgAlaValPro	480
DB	1452	CTGAGCACCCAGCAGGCCCTCACCAGAGAGTGGTGTCTCTGCACAGGGCTGTGCC	1511
QY	481	LysAspIysTrpValLeuAsnHisGluAspLeuValLeuGlyGluGlnIleGlyArgGly	500
DB	1512	AAGGACAAGTGGTGTGTGAACCATGAGGACCTGGTGTGGGTGAGCAGATTGGACGGGG	1571
QY	501	AsnPheGlyGluValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaValLys	520
DB	1572	AACTTTGGCGAGTGTTCAGCGGACCGCTCGGAGCGCCACCAACCCCTGGTGGCGGTGAAG	1631
QY	521	SerCysArgGluThrLeuProProAspLeuLysAlaLysPheLeuGlnGluAlaArgIle	540
DB	1632	TCCTTGTGAGAGAGCGCTCCACCTGACCTCAGGCCCAAGTTTCTACAGGAAGCGAGGATC	1691
QY	541	LeuLysGlnTyrSerHisProAsnIleValArgLeuIleGlyValCysThrGlnLysGln	560
DB	1692	CTGAAGCAGTACAGCCACCCCAACATCGTGGCTCTCATTTGGTGTGTGCACCCCAAGAGCAG	1751
QY	561	ProIleTyrIleValMetGluLeuValGlnGlyAspPheLeuThrPheLeuArgThr	580
DB	1752	CCCATCTACATCTCATGGAGCTTGTGCAGGGGGGCGACTTCTCTGACCTTCTTCCCGCAGC	1811

Qy	581	GluclyAlaArgLeuAroVallysThrLeuLeuGlnMetValclyAsAlaAlaGly	600
Db	1812	GAGGGGGCCGGCTCGGGGTGAAGACTCTGCTGCAGATGTTGGGGATGCAGCTCTGGC	1871
Qy	601	MetGluTyrLeuGluSerIysCysYllleHisArgAspLeuAlaAlaArgAenCysLeu	620
Db	1872	ATGGAGTACCTGGAGAGCAAGTCTGCATCCACCGGGACCTGGCTGCTCGAACTGGCTG	1931
Qy	621	ValThrGluIysAsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAlaAsp	640
Db	1932	GTGACAGAGAAGAATGTCTGAAGATCAGTGACTTTGGGATGTCCCGAGAGGAAGCCGAT	1991
Qy	641	GlyValTyrAlaAlaSerGlyGlyLeuArgGlnValProVallysTyrThrAlaProGlu	660
Db	1992	GGGGTCTATTGCAGCGCTCAGGGGGGCTCAGACAAGTCCCGCTGAAGTGGACCGCACCTGAG	2051
Qy	661	AlaLeuAsnTyrGlyArgTyrSerSerGluSerAspValTrpSerPheGlyIleLeuLeu	680
Db	2052	GCCCTTAACCTACGGCGCGCTACTCTCCGAAGACACGCTGTGGAGCTTTGGCATCTTGGCTC	2111
Qy	681	TrpGluThrPheSerLeuGlyAlaSerProTyrTrpAsnLeuSerAsnGlnGlnThrArg	700
Db	2112	TGGGAGACTTTCAGCGCTGGGGGGCTTCCCGCTATCCCAACCTCAGCAATCAGCAGACACGG	2171
Qy	701	GluPheValGluLysGlyGlyArgLeuProCysProGluLeuCysProAspAlaValPhe	720
Db	2172	GAGTTTGTGGAGAAGGGGGGGCGTCTGCCCTGCCAGAGCTGTGCTCTGATGCCGGTTC	2231
Qy	721	ArgLeuMetGluGlnCysTyrAlaTyrGluProGlyGlnArgProSerPheSerThrIle	740
Db	2232	AGGCTCATGGAGCATGTCTGGGCTTATGAGCTGGGACGGCGCCAGCTTCAGCACCATC	2291
Qy	741	TyrGlnGluLeuGlnSerIleArgIysArgHisArg	752
Db	2292	TACCAGAGCTCAGAGCATCCGAAGGGGCATCGG	2327

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RESULT 3
US-09-817-180-3
; Sequence 3, Application US/09817180
; Patent No. 6340594
; GENERAL INFORMATION:
; APPLICANT: GAN, weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01183
; CURRENT APPLICATION NUMBER: US/09/817,180
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15297
; TYPE: DNA
; ORGANISM: Human
US-09-817-180-3

Alignment Scores:
Pred. No.: 2,55e-198 Length: 15297
Score: 2137.00 Matches: 747
Percent Similarity: 21.28% Conservative: 0
Best Local Similarity: 21.28% Mismatches: 5
Query Match: 55.09% Indels: 2764
DB: Gaps: 16

US-10-660-763-2 (1-752) x US-09-817-180-3 (1-15297)

Qy 1 MetGlyPheSerSerGluLeuCysserProGlnGlyHisGlyValLeuGlnMetGln 20
Db 2563 ATGGGCTTCTCTTCTGAGCTGTGCAGCCGCCACGGGGCCCTCTGCGAGCAATGCGAG 2621
Qy 21 GluAlaGluLeuArgLeuGluGlyMetArgLysTrpMetAlaGlnArgValLysSer 40
Db 2623 GAGGCCGAGCTTCGTCTACTTGGAGGGCATGAGAAATGATGGATGGCCCGGGGTCAAGAGT 268

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QY 129 ----- 129
Db 3762 TGGGCCCATTTTATAAAGTTTCTGGAAACACAGCTATGCCCCCTTTGTTTCATATTGT 3821
QY 129 ----- 129
Db 3822 CTGTGACTACAATGACAGAGTTGAGTAATTGTGACAGAGGCTCTATGGCCTACAAAGCCTA 3881
QY 129 ----- 129
Db 3882 AAATAATTATTTACTATCTGCCCCCTTAAGAAAAAGACTGATCTAGTCGAGGAATCTAGC 3941
QY 129 ----- 129
Db 3942 TCAGTTACAGATGGGAAACTGAGGTTGGGGCTTGCCCAACATATCCCAGACATAAAC 4001
QY 129 ----- 129
Db 4002 AGGAGAACTGGACGAGAACACTGATCTCGGGCTGTCTATTCCTACTGCCAAGAACA 4061
QY 129 ----- 129
Db 4062 TAATTTGCAGGACCCAGTCAGTCAAGTGAATTTGTGGGGTCTTTGTTAAAGATTGCTAGG 4121
QY 129 ----- 129
Db 4122 AATTTCCAGGTGGCAATTAATGGAGAATGAACCAAGCACAGGGCCCTTTACATGTGGAG 4181
QY 129 ----- 129
Db 4182 CCCGCTGTACTGACAGGGCGTGACACCTGCAACTGGGCCCTGCTGCCACCGGTAC 4241
QY 129 ----- 129
Db 4242 CACTGTCAAGGAGGACCGTTGTAGCTGTAGTCTACCTCTTTGCTCCCAAG 4301
QY 129 ----- 129
Db 4302 GGTCGTCTTCAACAGGCTCTCTGATCTTTGACTCTCACGTGACAGCCAGCTTTCCAG 4361
QY 129 ----- 129
Db 4362 AAGTCTCAGGTGCTCTTGGCTGACAGCAGGACCTTTCAGGGCTTCACCCCGGCAAG 4421
QY 130 -----ThrHi 131
Db 4422 AATCTCCACAACTGGGGACCTGTGCTCCCCACACTGGCCTCTCTCTCTCCCTAGACCCA 4481
QY 131 sSerGlnAspIleGluLysLeuLysSerGlnTyrArgAlaLeuAlaLysAspSerAlaG1 151
Db 4482 CAGCCAGGACATTGAGAAGCTGAAGAGCCAGTACCGAGCTCTGGCACGGACAGTGCCCA 4541
QY 151 nAlaLysArgLysTyrGlnGluAlaSerLys----- 161
Db 4542 AGCCAAAGCAAGTACCAGGAGGCCAGAAAGTTTCGTGCTCCCTTGTGGCAGGGAG 4601
QY 161 ----- 161
Db 4602 GGAATCCGAAGCCAGTGTGACCTGTCTTTGGGTACCAGAGAGTGGGGCTGCTGGGC 4661
QY 162 -----AspLysAspArgAspLysAl 168
Db 4662 CTCCATGCTGTACTATACCCCTTGCCCCCTTCTGGCAGACAAAGGACCGTGCAAGGC 4721
QY 168 aLysAspLysTyrValArgSerLeuTrrpLysLeuPheAlaHisHienArgTyrValLe 188
Db 4722 CAAGGACAAGTATGTGGCAGCCTGTGGAAGCTCTTTGCTCACCACCAACCGCTATGTGCT 4781
QY 188 uGlyValArgAlaAlaGlnLeuHisHisGlnHisGlnLeuLeuLeuProGlyLe 208
Db 4782 GGGGCTGGGCTGCGCAGCTACACCAGCACCACCAGCTCTCTGCTGCCCGCCT 4841
QY 208 uLeuArgSerLeuGlnAspLeuHisGluGluMetAlaCysIleLeu----- 223

Db 4842 GCTGCGGTCACTCAGGACCTGCACGAGGAGATGGCTTGTCATCTCTGTAAGCCCCCAGCCC 4901
QY 223 ----- 223
Db 4902 CGTCCCTTGCCCCCACCCTTGAGCAGCCCTAAGCCCGCCATCAGSCCCAGAGGCAGGA 4961
QY 223 ----- 223
Db 4962 CCAGAAAAATCCATTGCTGGGAAGGTGCTGCCCATGTAAACCACATGAGAACGGACCTGG 5021
QY 223 ----- 223
Db 5022 GCCAAGATTGGAACAGGCAACTTACCTCTGAATTTACACTATTCAGGGTCTCATTTATT 5081
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Db 5082 CCAGGGTTTTTATTACATTCATTGAGCACTGTTCTGGGCTCTGGATTATACCAGAGAACGA 5141
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Db 5142 TGGTAGACAAAAACATCTGTCTCAGGGATCTTTTCGTGTTAGTGGAGTGAGAATGTGAGG 5201
QY 223 ----- 223
Db 5202 AGCACTAAGACCATGGAGAAAAATAAAGCAAGAGAAGTGGATCGGGACCTGGGAGCACG 5261
QY 223 ----- 223
Db 5262 GAGCAAGGGAGGAGGTGACAGTTTGTCATAGAGTGTATCTGGGNAAGCCTCTTGAGAGGT 5321
QY 223 ----- 223
Db 5322 GACATTCAAAAGAGCCCTGAGAGGGGTACGGAGTGAATCATGGGGCTATTTGGAGAAA 5381
QY 223 ----- 223
Db 5382 GACCATTCAGAAAGGAGGACAGCAATTTACAGGCCCTTGAGGTAGGAGAGTACCAGGA 5441
QY 223 ----- 223
Db 5442 CTAAATAGCCAGGAACCAAGTGGTGCCTCTGAGAGTGAGGGAGGGGAGAGTCATACACGAG 5501
QY 223 ----- 223
Db 5502 GCTGGAGAGGACGGGCTCAAGGGCTACTGGGTGATAGAAGGTCTAGCAGGGCCATGGTG 5561
QY 223 ----- 223
Db 5562 AGGACTTTGGCTCTGGGTGAACAAGAAATGGCATGATCTGACCTCTGTTTTTTTGTTCAT 5621
QY 223 ----- 223
Db 5622 TTTGTTTTAACTTTTTTTGAGTCAGAGTCTCGCTCTGCCGCCAGGCTAGAGTGCAGTGG 5681
QY 223 ----- 223
Db 5682 CATGATCTCGGCTTACTGCAACCTCCGCTCCAGGTTCAAGTGAATTCCTCCCTGCTCAGC 5741
QY 223 ----- 223
Db 5742 CTCCGAGTAGCTGAAACTACGGGCATGCGCCACACACACCAAGCTAATTTTGTATTTT 5801
QY 223 ----- 223
Db 5802 AGTAGAGCGGGTTTTCAACATGTTGCCCAGGCTAGTCTCTAATTTCTGGGCTCAAAAGCG 5861
QY 223 ----- 223
Db 5862 ATTTGCTGCTCTGCTCTCCAAAGTCCCGGATTACAGSCATGAGCCACCATGCCCAGC 5921
QY 223 ----- 223

D	b	5922	CCTGACCTCTGTTTAAATAAGGCCACTCTGGCTGCTGTGCTGCAAAATAGACTTCAAGGAG	5981
Q	y	223	-----	223
D	b	5982	CAAGCACAGAAGCTGGGAGGCCAGAGACGAGCTGTTGCCATAATCCAGATCCAGCTT	6041
Q	y	223	-----	223
D	b	6042	TTGGCCAGCTAGGACGGGGAGGTAGCAATGAGGTGAGGCGCGGTCAAGTCTCTGGGGCAG	6101
Q	y	223	-----	223
D	b	6102	GTCTCGAAAGGTGAAGCCAGCTGGGATTTCCCTATGGAATTGGAAGTGGGGCGTGAAATAGA	6161
Q	y	223	-----	223
D	b	6162	GGAGTCAGGGGTCACTCTCGGGATTTGGCTGGAGCAGCTGGAAGATGGAGTGGCTGTTA	6221
Q	y	223	-----	223
D	b	6222	ACTTATGTAGGAAGGCTGTGGGAAGAAGAGTTTAGGAGACAAGGATAGCAGTTCATTT	6281
Q	y	223	-----	223
D	b	6282	ATTTATTTATTTATTTATTTATTTATTTATTTATTTAGAGATGTAGTCTCATTTCTTCGC	6341
Q	y	223	-----	223
D	b	6342	CAGGCTGGAGTCAGTGGCGGATCTTGGCTCAGTCGAACCTCCACCTCCAGGCTCAAG	6401
Q	y	223	-----	223
D	b	6402	CGATTCCTTCGCTCAGCCTCCGAGTAGCCAAAGTAGCTGGAGCTACAGGCATGTGCCAC	6461
Q	y	223	-----	223
D	b	6462	CATGCTCGCTAAATTTTGTATTTTGTCTTTTTCAGTAGAGATGGGGTTTCCACACGTTAGC	6521
Q	y	223	-----	223
D	b	6522	CAGGCTGGTCTCGAACTGACCTCAGGCAATCCACCGCTCGACCTCCAGTGTGGTAT	6581
Q	y	223	-----	223
D	b	6582	TATAGCGTGAGCCACTGTGCTGGCCCACTGGATCCTTATTAACAAGTGCAGTGTCCCT	6641
Q	y	223	-----	223
D	b	6642	CTTATATATATCAGGAATAGAGATTAGGAGAGGTTAAATAATTTCCTAGAGTGGCA	6701
Q	y	223	-----	223
D	b	6702	TGGCTAGCTCGAAGTGAGCGAGGGTCAACCCAGCCCTGACTCCAACCCAGGTCCTA	6761
Q	y	223	-----	223
D	b	6762	GGCCTGAACTGCCAGCCTTGCCAGCTGAGGCTCCCTGACTGGGATCCCGTCTCG	6821
Q	y	224	-----LysGluIleLeuGlnGluTyrlleuGluIleSerSerIleuValGlnAspGluVal	241
D	b	6822	GGGCAGGAGGAGATCCTCGAGAAATACCTGGAGATTAGCAGCTGTGTGAGGATGAGGT	6881
Q	y	241	lValAlaIleHisArgGluMetAlaAlaAlaAlaArgIleGlnProGluAlaGluTy	261
D	b	6882	GGTGGCCATTCAACGGGAGATGCTGCAGCTGCTCCCGCATCCAGCCTGAGGCTGAGTA	6941
Q	y	261	rGlnGlyPheLeuArgGlnTyr-Gly-----	269
D	b	6942	CCAAGGCTTCTCGACAGATATGGTAAAGCCCGCTTGTCTGTGCTGGGCCCCAGGGCT	7001
Q	y	270	-----SerAlaProAspValProProC-----	277
D	b	7002	GCTGGCTGTGCCACTGACGGGGCGGTGTCCCCCAAGGTCGACCTCAGCTCCACCTC	7061

Qy	277	yValThrPheAspGluSerLeuLeuGluGlyGluProLeuGluProGlyGluLeuG	297
Db	7062	GTTGTACAGCTTCATGAGTCACTGCTTGAGGAGGGTGAACCGCTGGAGCCTGGGAGCTCC	7121
Qy	297	InLeuAnsGluLeuThrValGluSerValGlnHisThrLeu-----	310
Db	7122	AGCTGAACGAGCTGACTGTGGAGAGCGTGCAGCACACGTG-GGTGGTGGCTTTGACCTG	7180
Qy	310	-----	310
Db	7181	GGCTGGCGGGGCTCCCAGCAGACCACGAGTGTATTATGTAGCAGGGCTAGTTCGTGGA	7240
Qy	310	-----	310
Db	7241	GACTGTCCACAGAGCTGTCAACAGGTGGCGGGCTTGTGTGGCTCTACAGGGATGCAC	7300
Qy	310	-----	310
Db	7301	TGGACCTGGGTTGAGGGGCGAGAGGGCTCGGTTCTAATGCTGCCCTCTCTTTGGGTGCA	7360
Qy	311	-----ThrSerValThrAspGluLeuAlaValAlaThrGluMetValPheArgArgGlnG	329
Db	7361	GGCTGACCTCAGTGACAGATGAGCTGGCTGTGGCCACCGAGATGGTGTTCAGGCGGCGG	7420
Qy	329	IuMetValThrGlnLeuGlnGlnLeuLeuArgAsnGluGluAsnThrHisProArgG	349
Db	7421	AGATGGTTACGCAGCTGCACAGAGAGCTCCGGNATGAGAGAGAGAACACCCACCCCGGG	7480
Qy	349	Iu-----	349
Db	7481	AGCGGTGNGTGGGCCCCCTGCTGCAGAGCCTCCTGGGCTCCCTCCCTCCTACTACCC	7540
Qy	349	-----	349
Db	7541	TAACTGTCTGGCTAGCCGCGCAGACGAGCCCTTATTCTTCATCCACCTCCACCC	7600
Qy	350	-----ArgValGlnLeuLeuGlyLysArgGlnValLeuGlnGlnAlaLeuGln	365
Db	7601	GCCCTGCTCGACGGGTGACGTCTGGGCAAGAGCAAGTCTGTCAAGAAGCACTGCAG	7660
Qy	366	GlyLeuGlnValAlaLeuCysSerGlnAlaLysLeuGlnAlaGlnGlnLeuLeuGln	385
Db	7661	GGCTGTGAGGTAGCGCTGTGCAGCAGGCCCAAGCTGCAGCCACGACGAGTGTGTGCAG	7720
Qy	386	ThrLysLeuGluHisLeuGlyProGlyGluProProValLeuLeuGlnAspAsp	405
Db	7721	ACCAAGCTGGAGACCTGGGCCCCGGCGAGCCCCGCTGTGTCTCTGTGAGGATGAC	7780
Qy	406	ArgHisSerThrSerSerSer-----	412
Db	7781	CGCCACTCACGTCGCTCCTC-GGTGAGCTGCCCATCCGGCGCGCTGCGCCGACCGGC	7839
Qy	412	-----	412
Db	7840	CTGCCACCTGGGCTGGCTCCTCATTTTTGCCCTCCCTCCCTAAGCCTGGCCACCC	7899
Qy	413	-----GluGlnGluArgGluGlyArgThrProThrLeu	424
Db	7900	GCTGACGTCTGTCCTGGCCTCAGGAGCAGGAGGGGGAGAGACACCAACGCTG	7959
Qy	425	GluIleuLysSerHisIleSerGlyIlePheArgProLysPheSer-----	440
Db	7960	GAGATCTTAAGAGCACATCTCAGGANATCTTCGCCCCCAAGTTCTCGGTGAGTGGCGCC	8019
Qy	440	-----	440
Db	8020	CAGCCTGGGCCCCCTACTGTGTGTTTCGAGTTTAAATCATCTGGGATGTCCTAGAGAGGA	8079
Qy	440	-----	440
Db	8080	GGCTCTCCGAGGCTGTTGTTATGGAGAGTTCTCTCTTCCCTGGGATTCAGGCTGCA	8139

QY 440 ----- 440
Db 8140 GATGTCCAGACCTGCCCCGTGTGACCCCTCCCTTCCATGCCCCCAGTGTGCTAAAGG 8199
QY 440 ----- 440
Db 8200 GACCAGCAACCTCGACTATTCCATGGCTCTCCCTGCTTCAGAGGGGTGGGGCCCTGTG 8259
QY 440 ----- 440
Db 8260 GCCTGGAGGAGGAGCACAGCTTGGTTTGGGTCTTCCCTGGGCTTCCCTTCCAG 8319
QY 440 ----- 440
Db 8320 CTCTGCCAGCGTGAGCCTGGGCCAGTCCAGTGCCCACTCCAGGGGCTGTGGATGGCTC 8379
QY 440 ----- 440
Db 8380 TGCATGCCACTCCATGGTTGTAAGGGCTGAGGGCATATAGGGGGAGAGAGACCCCG 8439
QY 440 ----- 440
Db 8440 GCTGCCCCACGGCTCTTCAACAAGGTGGTTAAGTGACTCCTCTCGATCCTCCCTTGC 8499
QY 440 ----- 440
Db 8500 CCAAGTCCCTCCACCGCTGCAGCTCATTCGGAGGTGCAGAACCCCTGCGATGAGCAGCT 8559
QY 440 ----- 440
Db 8560 GTGTACCAGGGGCCATCCGAGGGCAGAGGTGGTGAGTGTGCTGCACTCTGGGA 8619
QY 440 ----- 440
Db 8620 CTTCTGTGTGGGAGAGCCAGGCAAGCAGGAGTACGTGTCTGGTGTGGATGG 8679
QY 440 ----- 440
Db 8680 TCTGCCCGGCACCTTCATCATCTCAGTCTTGATGTGAGTGTGGGCTGGACCCGAGCCTT 8739
QY 440 ----- 440
Db 8740 CCAGGCTCACTCTTCCCTCCCTTCCCTTCCCAAGGGAATGGCCTTTCAGGGTAGGG 8799
QY 440 ----- 440
Db 8800 GGTAGCTGCCAGGTCTTGGATGCCTCCTAGCAGGCTGGCTGGAAGGGCCACAGAGAC 8859
QY 440 ----- 440
Db 8860 CACCTGTCTGCAACAAAATAGAGGCTTAAGTGTGAGTCTCTCCCTGGTGGGGCAGCA 8919
QY 440 ----- 440
Db 8920 GGATGTATGTGCCATCAGATGGCATCTTTTCTGGAGGTCTCTGTGCCCTGGTCTCTGGG 8979
QY 440 ----- 440
Db 8980 CAGGCCCTTTCTCCCTGCTGCTCTCCTCTTCCCTCCAGGGCTCAGGCCCTCAGA 9039
QY 441 -----
Db 9040 ATGGAGGCTGTGACCCCGGTGCCCTGCCCTGCAGAACCTGTACCGACTGGAAAGGGAA 9099
QY 449 GlyPheProSerIleProLeuLeuIleAspHisLeuLeuSerThrGlnProLeuThr 468
Db 9100 GGCCTTCTAGCATCTCTTCTCTATGCACCACCTACTAGCACCCAGACCCCTCACC 9159
QY 469 LysLysSerGlyValValLeuHisArgAlaValProLys----- 481
Db 9160 AAGAAGAGTGTGTGCTCTGCACAGGGCTGTGCCCAAGGTGAGCCTGCACCCAGCCTGG 9219
QY 481 ----- 481

Db 9220 CCCATGCCACCTGTGGCAGGGCTTGGGAGTGTGGGTACAGGCCCAACCCAGCGTCTGAGCA 9279
QY 481 ----- 481
Db 9280 GAAAGGCTTTCCAGGGCCCTCCGTCTACATACAAGATGCAGAGTGAGTACCCCTCAGGGC 9339
QY 481 ----- 481
Db 9340 CAGCCTTGCTTAGGTTTGAATGTACAGGCCACTCTCTATGCCATGGGCTGTACACACCA 9399
QY 481 ----- 481
Db 9400 GGTGTGCTTACTCTGTGTCAGGGACCTGCTGCACCCCGTAGTCATCTCAGTGTGCTCC 9459
QY 481 ----- 481
Db 9460 CCAGTGGTCCCACCCCTGTGTACATATGAGGGCGCCAAAATAATGGAGGACACAGCCCTT 9519
QY 481 ----- 481
Db 9520 CTAAGGGCCACAGCACCCCTTTTCTTCAGACTTCTGATCCCTGTCTCTCTTCCCCAG 9579
QY 482 AspLysTrpValLeuAsnHisGluAspLeuValLeuGlyGluGlnIleGlyArg----- 499
Db 9580 GACAAGTGGTGTCTGAACCATGAGGACCTGGTGTGGGTGAGCAGATTGGACG--GGTGAG 9638
QY 499 ----- 499
Db 9639 TGGCCCTCTGCTGGCTCTTGTGCTGGGACTTCTCTCTGAGTCTGGGCTGGGCCCTT 9698
QY 499 ----- 499
Db 9699 GCCTTACACCCAGAAACCTCCTGCCCCATCTGATTTCCCACCTTGTACCCGACTCCCT 9758
QY 499 ----- 499
Db 9759 GCCAGGCCCCACACACACCATCTCTCCAGAAACGGGACAGTACCTACGCTGAAACTC 9818
QY 499 ----- 499
Db 9819 CCAGCAGACAGCTCTGCGACACCCCTGACCTCATCACCACCCAGCCGCCCCCATCG 9878
QY 499 ----- 499
Db 9879 AGCTCTTGTGTGCACGCGAGGAGACACCTGTTACTGTAAAGCCATAAGATACCTGTTTAG 9938
QY 499 ----- 499
Db 9939 GGAAGAAGTCACTGTCTTAAATACAGATGCTTTTCAAACCCCAAGGAGAGTATTTT 9998
QY 499 ----- 499
Db 9999 GGATTTCCATGTCACTTCTCTCAGGAAGGGTGGCACATCGAGGCAACTTTTCCCTGCTG 10058
QY 499 ----- 499
Db 10059 CCCCATGTGCTCTAGGTTTCCCAGCGAGGGTCAAACTCCACAGAGACCTGGGTGGAGG 10118
QY 499 ----- 499
Db 10119 GTCCGAAACAGGGGGCCCTCACCAGGGGTAGGAAGCAGATGGGTAGGAAGCGGAGA 10178
QY 500 -----
Db 10179 AGAGAACTCGGGACTGGGAAGGCCGTGGTAGGAGCCCAAGACCGTTTTCAGGGGAACCTT 10238
QY 503 GlyGluValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaValLysSerCys 522
Db 10239 GCGAAGTGTTCAGCGGACGCTGCGAGCGGACACACACCTGGTGGCGGTGAAGTCTTGT 10298
QY 523 ArgGluThrLeuProAspLeuLysAlaLysPheLeuGlnGluAla----- 538
|||||

Db 10299 CGAGAGCGCTCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCAGGTGGGTGATA 10358
 Qy 538 ----- 538
 Db 10359 AACTAATGATACACCAGCGGTCCCGGATACACAGAGGTTACACTGCATGCCACAGTGTGAA 10418
 Qy 538 ----- 538
 Db 10419 GTGCTTGACCAACGTTGGTGTGTTAGTCTCTGAGGCCGCCATTCGCGGTAGTACCCCC 10478
 Qy 538 ----- 538
 Db 10479 TTATAGTGCAGAGGTAGAGGTGCCCAGGTACACGTCGCGGTCTGCTGGCCTTGA 10538
 Qy 538 ----- 538
 Db 10539 GGCCAGCTCTTCCCATCATCCCTGGGGGCCCTGGGAGCGCGGCTGGCCACGTAG 10598
 Qy 539 -----ArglleLeuLysGlnTyrSerHisProAsnIleValAr 551
 Db 10599 ATCCTGAGCAGAGTGCCTCCAGGATCTCTGAAGCAGTACAGCCACCCCAACATCGTGCG 10658
 Qy 551 gLeuIleGlyValCysThrGlnLysGlnProIleTyrIleValMetGluLeuValGln-- 570
 Db 10659 TCTCATGGTGTCTGCACCCAGACGACCCATCTACATCGTCTATGGAGCTTGTGCAGGG 10718
 Qy 570 ----- 570
 Db 10719 TGAGCGGGGCGCTGAGCTCCAGGTAGGGCGCGCAGCCTGGTCAAGTGGCAGCCTTACC 10778
 Qy 571 -----GlyGlyAspPheLeuThrPheLeuAr 579
 Db 10779 TCAGAGGCTCAGCAGGGGCTCCTCCACCTGCGAGGGGGGACTCTCTGACCTTCCTCCG 10838
 Qy 579 gThrGluGlyAlaArgLeuArgValLysThrLeuLeuGlnMetValGlyAspAlaAlaI 599
 Db 10839 CACGAGGGGGCCCGCTCGGGTGAAGACTCTGCTCAGATGTTGGGGATGAGCTGC 10898
 Qy 599 aGlyMetGluTyrLeuGluSerLysCysIleHisArg----- 612
 Db 10899 TGGCATGGAGTACCTGAGAGCAAGTGTGATCCACCG-GTGAGTGGCGGTGGCCACG 10957
 Qy 612 ----- 612
 Db 10958 GGCCCTGCCAACACCCCGCAGAGTCAAGAGGTACCTATACCCCTAGGGCCCCCGCT 11017
 Qy 612 ----- 612
 Db 11018 GGACCATCAGGCATCAGCTCCAGAGGGGAGTTGGCCCTCTGTGTGTAGACAGGGGTGCCA 11077
 Qy 612 ----- 612
 Db 11078 GGGCCGGGAGCAGCTTTTGTCTTGGCTTTCCTAGAGTGTTCAGCCAGGGCTGGCAGGC 11137
 Qy 613 -----AspLeuAlaAlaArgAsnCy 619
 Db 11138 GACTGTTGGCCAAATGAGCCCTGCTCTCACCAGGACCTGGCTGCTCGAAGCTG 11197
 Qy 619 sLeuValThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluAlaI 639
 Db 11198 CCTGGTGACAGAGAAGTGTCTGAAGATCAGTACTTGGATGTCCTCCGAGAGGAAGC 11257
 Qy 639 aAspGlyValTyrAlaAlaSerGlyLeuArgGlnValProValLysThrAlaApr 659
 Db 11258 CGATGGGCTATGACGCTCAGGGGCTTCAGACAAGTCCCGCTGAAGTGGACCGCAC 11317
 Qy 659 oGluAlaLeuAsnTyr----- 664
 Db 11318 TGAGGCCCTTAACCTACGTTACCTGCTACCTGGACTCCATGGCCAGAGGCCA 11377
 Qy 664 ----- 664
 Db 11378 GGCCTGGGTCTCGCGGTGCTCGCTCGCCCGCCAGGGAGGTGCACTACGCTGCCTC 11437

Qy 665 -----GlyArgTyrSerSerGluSerAspValTrpSerPheGlyI 678
 Db 11438 ACTCTCCGCTCCTCTGTCAGGCGCTACTCTCCGAAAGCAGCTGTGGAGCTTTGGCA 11497
 Qy 678 lLeuLeuTrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnG 698
 Db 11498 TCTTGCTCTGGGAGACCTTTCAGCTGGGGGCTCCCTCTATCCCAACCTCAGCAATCAGC 11557
 Qy 698 lThrArgGluPheValGluLys----- 705
 Db 11558 AGACCGGAGTTTGTGGAGAGGGTAAGCACCTGTGATGACAGCAGCCTCAGGCTGCA 11617
 Qy 705 ----- 705
 Db 11618 CCCTCTTCCAGATGCTCCAGCGGACTCTTAACTCCCTTAATGCCAACCTTCCCAACA 11677
 Qy 705 ----- 705
 Db 11678 GGCAGATAAGAATAACCTGGCCAGTTGTCACGCCTGTCTATCCAGCACTTTTGGGAGGC 11737
 Qy 705 ----- 705
 Db 11738 TGAGCTGGTGGATCACTTTCAGCCAGAGGTTCAGATCAGCTTGGACAACACAGTGAAA 11797
 Qy 705 ----- 705
 Db 11798 CTCCATCTGTACAAAAAATAACAAATAGACTGGGCGAGGTGGCTCACACCTGTATATCCC 11857
 Qy 705 ----- 705
 Db 11858 AGACTTTGGGAGGCCGAGGAGGTGATCACCTGTGTGTCAGGAGTTTGTAGACCAAGCAG 11917
 Qy 705 ----- 705
 Db 11918 ACCAACATGTGTAAACCCCATCTCTACTAAAAATACAAAAATTAGCCAGGCATGGTGCCA 11977
 Qy 705 ----- 705
 Db 11978 CGTGCTGTATCCAGCACTACTTGGGAGGCTGAGTGGGAGAAATTGCTTGAACCCAGAG 12037
 Qy 705 ----- 705
 Db 12038 GCGGAGGTGCTAGTGAGCGCAGATTGTGCCACTCCAGCCTGGCGGACAGAGATGA 12097
 Qy 705 ----- 705
 Db 12098 AACTCCATCTCAAAAAAACCAAAAAACAAAAAATACAAAAATTAGCTGGGTGTGGTGAC 12157
 Qy 705 ----- 705
 Db 12158 ATGCGCTGTAGTCCCTGCTACTCGGGAGGCTGAGTGGGAGGATCCTGGAGCCCGGA 12217
 Qy 705 ----- 705
 Db 12218 GGTGGAGTTGTCAGTGAGTGAATCATGCCACTGCACCCCAACCTGGGTGACAGAGAGA 12277
 Qy 705 ----- 705
 Db 12278 GAGAGAGCCTTGACTCGAAAAAAGAAAAAACCTGGGCGCAGTGGCTCAGCCTGTAAAT 12337
 Qy 705 ----- 705
 Db 12338 TCAACATTTTGGGAGGCTGAGGAAGTGGATCATCTTAGTCTAGGAGTTTGACACTAGCC 12397
 Qy 705 ----- 705
 Db 12398 TGGCCAACTGGCAAAACCTGTCTCTACTAAAAATACAAAAAATTAGCGAGGTGTAGTG 12457
 Qy 705 ----- 705
 Db 12458 TGCAAGCTGTAAATCCAGCTACTTTGGAGGCTGAGGCAAGNATCGCTTGAACCTGGG 12517

Qy	129	-----	129	Db	4782	GGCGTGGCGCTGCGCAGCTACACCCAGCACCCACCACTCTCTGCTCCGCGCT	4841
Db	3702	CGGCCCTGGTGGCCACCCCTGGCCCATTCCTCGCCCAAAAGATCATCTGATTCAGGG	3761	Qy	208	uLeuA-rsSerLeuGlnAspLeuHisGluGluMetAlaCysIleLeu-	223
Qy	129	-----	129	Db	4842	GCTGCGTCACTGCGAGACCTGCACGAGGATGGCTTGCAATCTGTAAAGCCCGCAGCCC	4901
Db	3762	TGGGCCCAATTTTATAAGTTTTTGTCTGGAACAACAGCTATGCCCCCTTTGTTTCATATTGT	3821	Qy	223	-----	223
Qy	129	-----	129	Db	4902	CGTCCCTGCGCCCCCACCCTTGAGCAGCCCTTAAGCCAGCCATCAGGCCAGAGGAGGAGGA	4961
Db	3822	CTGTGACTAATGACAGAGTTGAGTAATGTGACAGAGGCTCTATGGCTTACAGCCTA	3881	Qy	223	-----	223
Qy	129	-----	129	Db	4962	CCCAGAAAATCCATTTGCTGGGAAGTGTGSCCATGTAACCATGAGAACGGGACCTGG	5021
Db	3882	AAATAITTTATTACTATCTGCGCCCTTTAAGAAAAAGACTGATCTAGTCGAGAACTTAGC	3941	Qy	223	-----	223
Qy	129	-----	129	Db	5022	GCCAAGGATTGGAAAACAGGCAACTTACCTCTGAATTACATATTCCAGGGTCTCATTTATT	5081
Db	3942	TCAGTTACAGATGGGAAACTGAGGTTGGCGGCTTGCCCAACATATCCAGCACATAAAC	4001	Qy	223	-----	223
Qy	129	-----	129	Db	5082	CCAGGGTTTTTATTACATTTGAGCAGCTGTCTCTGGGCTCTGGATTTATACAGAAACGA	5141
Db	4002	AGGAACTGGACGAGAACACTGATCTCGGGCTGTCTATCTATTCCTACTGCCAAGAACA	4061	Qy	223	-----	223
Qy	129	-----	129	Db	5142	TGGTAGACAAAAACATCTGTCTCAGGGATCTTTCGTGTAGTGGAGTGAGATGTGAGG	5201
Db	4062	TAAATTTGCAGGACCCAGTGCAAGTGAAATTGTGGGGTCTTTGTTAAAGATTGCTAGG	4121	Qy	223	-----	223
Qy	129	-----	129	Db	5202	AGCACTAAGACCATGGAGAAAAAATAAGCAAGAGAGTGATCGGACCTGGGAGCAGC	5261
Db	4122	AATTTCCAGTTGGCAATAATAGGAGATGAAACCAAGCAGGAGGCTTCTACATGTGGAG	4181	Qy	223	-----	223
Qy	129	-----	129	Db	5262	GAGGCAAGGAGGAGGTGACAGTTGTCATAGAGTGATCTGGGAAAGCCTCTTGAGAGGT	5321
Db	4182	CCCCGTGTGACTGCACAGCGCTGCACACCTGCAACTGGGCTGCTGCCACGAGGCTAC	4241	Qy	223	-----	223
Qy	129	-----	129	Db	5322	GACATTTCAAAGAGGCCCTGAGAGGGTACGGAGTGAATCATGGGGCTATTTGGAGAAA	5381
Db	4242	CACTGTAGTCCAGGAGGAGCCGTTGTAGCTGTAGTCTACCTCTTTGGCTCCCAAGG	4301	Qy	223	-----	223
Qy	129	-----	129	Db	5382	GACCATTCAGAAAGGAGGACAGCAATTACACAGCCCTTGAGTAGGAGAGTACCGAGGA	5441
Db	4302	GGTCTGTCTTCAACAGGCTCTGTGATCTTTGACTCTACGTCTCAGCAGCAGCCTTTCCAG	4361	Qy	223	-----	223
Qy	129	-----	129	Db	5442	CTAATAGCCAGGAACCACTGGTGGTCCCTCTGAGAGTGAGGAGGGGAGAGTACATACACG	5501
Db	4362	AACTCTCCAGGTCTCTTGCTGCTGACGACAGACCTTTCCAGGGCTTCAACCCAGGCAAG	4421	Qy	223	-----	223
Qy	130	-----	ThrHi 131	Db	5502	GCTGGAGGAGGAGGCGCTCAAGGGCTACTGGGTGATAGAAGGTCTAGCAGGGCCATGGTG	5561
Db	4422	AATCTTCCAACTGGGGACCTGCTGCCCAACACTGGGCTCTCTCTCTCTCCCTAGACCCA	4481	Qy	223	-----	223
Qy	131	sSerGlnAspIleGluLysLeuLysSerGlnTyrArgAlaLeuAlaArgAspSerAlaG1	151	Db	5562	AGGACTTTGGCTCTGGGTGAAACAGAAATGGCATGATCTGACCTCTGTTTTTTTGTTCAT	5621
Db	4482	CAGCCAGGACATTTGAGAAGCTGAAGAGCAGTACCGAGCTCTGGCAGCGGACATGTCCCA	4541	Qy	223	-----	223
Qy	151	nAlaLysArgLysTyrGlnGluAlaSerLys	161	Db	5622	TTTGTTTTAACTTTTTTTTGATCAGAGTCTCGCTCTGCGCCCGCAGGCTAGAGTGCAGTGG	5681
Db	4542	AGCCAAAGCGCAGTACCAGGAGGCCAGCAAGAGTTGCTGGCTTCCCTTCTGCTGGCAGGAG	4601	Qy	223	-----	223
Qy	161	-----	161	Db	5682	CATGATCTCGGCTTACTGTGCAACCTCCGCTCCAGGTTCAAGTGATTTCCCTGCTCAGC	5741
Db	4602	GGAATCCGAAGCCAGTGTGACCTGCTTTGGGTACCCAGAGAGTGGGGCTGCTGGGC	4661	Qy	223	-----	223
Qy	162	-----	AspLysAspArgAspLysAl 168	Db	5742	CTCCCGAGTAGTGAAACTACGGGCATGCGCCACACACCCAGCTAATTTTGTATTTTT	5801
Db	4662	CTCATGCTGTATCTATACCCCTTGCCCCCTTCTGGCAGACCAAGGACCGTGACAAGGC	4721	Qy	223	-----	223
Qy	168	aLysAspLysTyrValArgSerLeuTyrLysLeuPheAlaHisHisAsnArgTyrValLe 188		Db	5802	AGTAGACGGGGTTTCCACCATGTTGCCCAGGGTAGTCTCTAATCTCTGGGCTCAAGCG	5861
Db	4722	CAAGGACAAAGTATGTGCGAGCTGTGGAAGCTCTTTGCTCACCACCAACCGCTATGTGCT	4781	Qy	223	-----	223
Qy	188	uGlyValArgAlaAlaGlnLeuHisGlnHisHisGlnLeuLeuLeuProGlyLe 208					

Db 5862 ATTTGCTGCTCTGCTCCCAAGTGC GGGAATTACAGGATGAGCCACCATGCCAGC 5921
Qy 223 -----
Db 5922 CCTGACCTCTGTTTAAATAAGGCCACTCTGGCTGCTGTGCTGCAAAATAGACTTCAGGGAG 5981
Qy 223 -----
Db 5982 CAAGGACAGAAGCTGGAGGCCAGAGAGCAGGCTGTTGCCATAATCCAGATCAAGCTT 6041
Qy 223 -----
Db 6042 TTGGCCAGCTAGGACGGGAGGTAGCAATGGAGGTGAGGCCGCTCAGGTCCTGGGCGAG 6101
Qy 223 -----
Db 6102 GTCTGGAAGGTGAAGCCAGTGGGATTTCCCTATGGAATTGGAACTGGGGCGTGAAATAGA 6161
Qy 223 -----
Db 6162 GGAGTCAGGGGTCACTCTGGGGATTGGCCCTGGAGCAGCTGGAAATGGAGTGGCTGTTA 6221
Qy 223 -----
Db 6222 ACTTATGTAGGAAGGCTGTGGGAAGAAAGAGGTTTAGGAGACAAGGATAGCAGTTCAATT 6281
Qy 223 -----
Db 6282 ATTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 6341
Qy 223 -----
Db 6342 CAGSCTGGAGTGAGTGGCGGATCTTTGGCTCACTGCAACCTCCACCTCCAGGCTCAAG 6401
Qy 223 -----
Db 6402 CGATTCTTCTGCTCAGCCTCCCGAGTAGCAAGTAGCTGGGACTAGAGGATGTGCCAC 6461
Qy 223 -----
Db 6462 CATGCTGGCTAATTTTGTATTTGCTTTTTCAGTAGAGATGGGTTTTCACCAGTTAGC 6521
Qy 223 -----
Db 6522 CAGSCTGGTCTCGAACTGACCTCAGGCAATCCACCGCCTCGACCTCCAGTGTGTAT 6581
Qy 223 -----
Db 6582 TATAGGCGTAGCCACTGTGCTGGCCCACTGGATCCTTATTACAACCTGCCAGTGTCCCT 6641
Qy 223 -----
Db 6642 CTTATATATACAGNAATAGNAGATTAGGAGAGGTTAAATAATTTGCTAGAGTGCCA 6701
Qy 223 -----
Db 6702 TGGCTAGCTCGAAGTGAGCAGGGGTCAACCCAGCCCTGACTCCAAACCCAGGGTCTTA 6761
Qy 223 -----
Db 6762 GGCTGAACCTGCCAGCCTTGGCCAGCCTGAGGCTCCCTGACTGGGGATCCCGTCTCGG 6821
Qy 224 -----
Db 6822 GGGCAGGAGGAGATCTGCAGGAATACCTGGAGATTAGCAGCCTGTGTGAGGATGAGGT 6881
Qy 241 lValAlaIleHisArgGluMetAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 261
Db 6882 GGTGCCATTCCACGGGAGATGGCTGACGTGCTGCCGCATCCAGCTCAGGCTGAGTA 6941
Qy 261 rGlnGlyPheLeuArgGlnTyr-Gly----- 269
Db 6942 CCAAGGGTTCTGCGACAGTATGGTAAAGCCCCGCTCTTGTCTGCTGGGCCCGAGGGCT 7001

Qy 270 -----SerAlaProAspValProProC 277
Db 7002 GCTGGCCTGTCCACTGACGGGGCGCTGTCCCCACACAGGTCCGCACCTGACGTCCACCCCT 7061
Qy 277 yValThrPheAspGluSerLeuLeuGluGluGluProLeuGluProGluGluLeuG 297
Db 7062 GTGTACGTTTCGATGAGTCACTGCTTGAGAGGGTGAACCGCTGGAGCGCTGGGAGCTCC 7121
Qy 297 iLeuAenGluLeuThrValGluSerValGlnHisThrLeu----- 310
Db 7122 AGCTGAACGAGCTGACTGTGGAGAGCGTGCAGCACACGTG-GGTGGTGGCTTTGCACCTG 7180
Qy 310 ----- 310
Db 7181 GGCTGGCGGGGCTCCACGACAGACACGAGTGTATATGTAGCAGGGCTAGTGTGGA 7240
Qy 310 ----- 310
Db 7241 GACTGTCCACACAGAGCTGTCAACAGGTGGCCGGCTTGTGTGGCTCTACAGGATGCAC 7300
Qy 310 ----- 310
Db 7301 TGSACCTGGGTTGAGGGGCGAGGGCTCGGTTCTTAATGCTGCCCTTCTCTTGGGTGCA 7360
Qy 311 -----ThrSerValThrAspGluLeuAlaValAlaThrGluMetValPheArgArgGlnG 329
Db 7361 GGCTGACCTCAGTGAACAGATGAGCTGGCTGTGGCCACCGAGATGGTGTTCAGGCGGCGAG 7420
Qy 329 lMetValThrGlnLeuGlnGlnLeuArgAenGluGluAenThrPheProArg 349
Db 7421 AGATGTTTACGACGTGCAACAGGAGCTCCGGAATGAAGAGGAGAACACCCACCCCGGG 7480
Qy 349 lu----- 349
Db 7481 AGCGGTGAGTGGGCCCTGCTGCAGCAGCCTCTCTGGCCCTCCCTCTCTACTACCTACCC 7540
Qy 349 ----- 349
Db 7541 TAACTGCTGTGCTAGCCCGCAGACCGAGCCCTTATTCTTCATCACCCCTCCACCC 7600
Qy 350 -----ArgValGlnLeuLeuGlyValArgGlnValLeuGlnAlaLeuGln 365
Db 7601 GCCCTGCTGTCAGGGTGCAGCTGCTGGCAAGAGGCAAGTGTGCAAGAGCACTGCAG 7660
Qy 366 GlyLeuGlnValAlaLeuCysSerGlnAlaLysLeuGlnAlaGlnGlnGlnLeuLeuGln 385
Db 7661 GGCTGCAGGTAGCGCTGTGCAGCCAGGCCAAGCTGCAGGCCAGCAGGAGTTGCTGCAG 7720
Qy 386 ThrLysLeuGluHisLeuGlyProGlyGluProProValLeuLeuLeuGlnAspAsp 405
Db 7721 ACCAAGCTGGAGCACCTGGGCCCGCGAGCCCGCTGTGTGCTGCTCTCTGCAGGATGAC 7780
Qy 406 ArgHisSerThrSerSerSer----- 412
Db 7781 CGCCACTCCAAGTGTGCTCTC-GGTGAGCTGCCCATCCGCGCGCGCTGCCCGCACCGGC 7839
Qy 412 ----- 412
Db 7840 CTGCCACCTGGGGCTGGGCTCTCTCATTTTCGCCCTCCCTCCCTAAGCTGGCCACCC 7899
Qy 413 -----GluGlnGluArgGluGlyArgThrProThrLeu 424
Db 7900 GCTGACGTCTGCTCCCTGGCCTCAGGAGCAGAGAGGGGGGGAAGGACACCCACGCTG 7959
Qy 425 GluIleLeuLysSerHisIleSerGlyIlePheArgProLysPheSer----- 440
Db 7960 GAGATCTTTAAGAGCCACATCTCAGGAATCTTCGCCCCCAAGTTCTCGGTGAGTGGCGCC 8019
Qy 440 ----- 440
Db 8020 CAGCCTGGGGCCCCCTACTGTTGTTTTCGAGTTTAACTACCTGGGATGCTCTAGAGAGGA 8079

10239	GCGGAAGTGTTCAGCGGACGCTGCGAGCGCAACACACCCTGTGTGGCGGTGAAGTCTTGT	10298	664	QY	664	-----	664
523	ArgGluThrLeuProAspLeuLeuAlaLeuPheLeuGlnGluAla	538	11378	Db	11378	GSCCTGGGTCTCGCGGCTGCTCGCCCTGCGCCACGAGGGTGCACCTCAGCTCGCCTC	11437
10299	CGAGAGCGTCTCCACCTGACCTCAAGCCCAAGTTCTACAGGACGAGGTGGGTGATA	10358	665	QY	665	-----GlyArgTyrSerSerGluSerAspValTrpSerPheGlyI	678
538	-----	538	11438	Db	11438	ACCTCTCGCCTCTCTCTCAGCGCGCTACTCTCCGAAAGGACGTGTGGAGCTTTGGCA	11497
10359	AACATAATGATCACCACCGGTCCGCGATACACAGAGGTTACACTGCATGGCACAGTGTGA	10418	678	QY	678	leuLeuTrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnG	698
538	-----	538	11498	Db	11498	TCTTCTCTGGAGACCTTCAGCCTTGGGGGCTCTCCCTATCCCACTCAGCAATCAGC	11557
10419	GTGCTTGACCACCGTGTGTGTGTAGTCTCGAGGCCCCCATTTGGGGTAGTACCCCC	10478	698	QY	698	InThrArgGluPheValGluLys	705
538	-----	538	11558	Db	11558	AGACACGGGAGTTTGTGAGAAGGTAAGCACCCCTGTGATCACAGCAGCCTCAGGCTGCA	11617
10479	TTATAGTCCGAGAGGTAGAGGTGCCCCAGGTCACACGTCCTCGGCTGTCTGCTGCTTGA	10538	705	QY	705	-----	705
538	-----	538	10539	Db	10539	GGCCAAGCTCTTCTCCATCATCTCTGGGGGCGCTGGGAGGCGGCGCTGGCCACGTAG	10598
10539	GGCCAAGCTCTTCTCCATCATCTCTGGGGGCGCTGGGAGGCGGCGCTGGCCACGTAG	10598	539	QY	539	-----ArgIleLeuLysGlnTyrSerHisProAsnIleValAr	551
539	-----	539	10599	Db	10599	ATCTGAGCAGCAGTGCCTCCAGGATCTTGAAGCAGTACAGCCACCCCAACATGTGGC	10658
10599	ATCTGAGCAGCAGTGCCTCCAGGATCTTGAAGCAGTACAGCCACCCCAACATGTGGC	10658	551	QY	551	gLeuIleGlyValCysThrGlnLysGlnProIleTyrIleValMetGluLeuValGln--	570
570	-----	570	10659	Db	10659	TCTCATTTGGTGTCTGCACCCAGAGCAGCCCATCTACATCTCATGTGAGCTTGTGAGGG	10718
570	-----	570	570	QY	570	-----	570
10719	TGAGCGGGGCGGTGAGCTCCAGGTAGGGCGCGCAGCCTGGTCAAGTGGCAGCCTTACC	10778	571	QY	571	-----GlyGlyAspPheLeuThrPheLeuAr	579
571	-----	579	10779	Db	10779	TCAGGAGGCTCAGCAGGGGTCTCCCCACCTGCAGGGGCGGACCTTCTGACCTTCTCCG	10838
10779	TCAGGAGGCTCAGCAGGGGTCTCCCCACCTGCAGGGGCGGACCTTCTGACCTTCTCCG	10838	579	QY	579	gThrGluGlyAlaArgLeuArgValLysThrLeuLeuGlnMetValGlyAspAlaAlaI	599
579	gThrGluGlyAlaArgLeuArgValLysThrLeuLeuGlnMetValGlyAspAlaAlaI	599	10839	Db	10839	CACGAGGGGCGCGCTCGGGTGAAGACTCTCTGCAGATGTTGGGGATGCACCTGC	10898
10839	CACGAGGGGCGCGCTCGGGTGAAGACTCTCTGCAGATGTTGGGGATGCACCTGC	10898	599	QY	599	aGlyMetGluTyrLeuGluSerLysCysIleHisArg-	612
599	aGlyMetGluTyrLeuGluSerLysCysIleHisArg-	612	10899	Db	10899	TGGATGGAGTACTGAGAGCAAGTCTGCTCATCCACCG- GTGAGTGGGCGGTGGCCACG	10957
10899	TGGATGGAGTACTGAGAGCAAGTCTGCTCATCCACCG- GTGAGTGGGCGGTGGCCACG	10957	612	QY	612	-----	612
612	-----	612	10958	Db	10958	GGCCCTGCCAACACCCCGACAGATCAAGAGGTACCTATACCCCTAGGGCCCCCGCT	11017
10958	GGCCCTGCCAACACCCCGACAGATCAAGAGGTACCTATACCCCTAGGGCCCCCGCT	11017	612	QY	612	-----	612
612	-----	612	11018	Db	11018	GGACCATCAGGCATCAGCTCCAGAGGGGAGTTGGCCTCTGTGTAGACAGGGGTGCCCA	11077
11018	GGACCATCAGGCATCAGCTCCAGAGGGGAGTTGGCCTCTGTGTAGACAGGGGTGCCCA	11077	612	QY	612	-----	612
612	-----	612	11078	Db	11078	GGGCGGGGAGCAGCTTTTGTCTTGGCTTCTTCTAGAGTGTTCAGCCAGGCTGGGCAGGC	11137
11078	GGGCGGGGAGCAGCTTTTGTCTTGGCTTCTTCTAGAGTGTTCAGCCAGGCTGGGCAGGC	11137	613	QY	613	-----AspLeuAlaAlaArgAsnCy	619
613	-----	619	11138	Db	11138	GACTGTTGGCCAAATGAGCCCTCCCTGCTCACCAGGAGGACCTGGCTCTCGGAACGT	11197
11138	GACTGTTGGCCAAATGAGCCCTCCCTGCTCACCAGGAGGACCTGGCTCTCGGAACGT	11197	619	QY	619	aLeuValThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluAlaI	639
619	aLeuValThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluAlaI	639	11198	Db	11198	CCTGGTACAGAGAAGAATGTCTTGAAGATCAGTGACTTTGGGATGTCCCGAGGGAAGC	11257
11198	CCTGGTACAGAGAAGAATGTCTTGAAGATCAGTGACTTTGGGATGTCCCGAGGGAAGC	11257	639	QY	639	aAspGlyValTyrAlaAlaSerGlyLeuArgGlnValProValLysTrpThrAlaPr	659
639	aAspGlyValTyrAlaAlaSerGlyLeuArgGlnValProValLysTrpThrAlaPr	659	11258	Db	11258	CGATGGGGTCTATGACGCTCAGGGGCGCTCAGACCAAGTCCCCGTGAAGTGGACCCACC	11317
11258	CGATGGGGTCTATGACGCTCAGGGGCGCTCAGACCAAGTCCCCGTGAAGTGGACCCACC	11317	659	QY	659	oGluAlaLeuAsnTyr	664
659	oGluAlaLeuAsnTyr	664	11318	Db	11318	TGAGGCCCTTAACTTACCGGTACCTAGTCCCTGTCTACCTCGACTCCATGCCACAGAGGCCA	11377
11318	TGAGGCCCTTAACTTACCGGTACCTAGTCCCTGTCTACCTCGACTCCATGCCACAGAGGCCA	11377	12039	Db	12039	TGGCCAACATGGCAAAACCTGTCTTCTACTAAAAATACAAAAATTAGCGAGGTGTAGTGG	12457

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QY 705 ----- 705
Db 12458 TGCAAGCTGTAATCCAGTACTTGGGAGGCTGAGGCACAGAATCGTTGAACCTGGG 12517
QY 705 ----- 705
Db 12518 AGGTGGAGGTTGAGTGAGCTGAGATCAACCACTGCATTCCAGCGTGGTGACAGACA 12577
QY 705 ----- 705
Db 12578 AGACTCCATCTCAGAAAAGAAAAAATAAGATATCCCTGTAGCTACTACTGAGTG 12637
QY 705 ----- 705
Db 12638 AGCACCTGGTCTGTGCTAGGTACATGTTATTTCAATTGCTCATCATATGTTGGTA 12697
QY 705 ----- 705
Db 12698 GGGATTAAATATGTCCTTTCTCAGATGGAAAAACAGCTGGCAGAGGGGACACAGTAGC 12757
QY 705 ----- 705
Db 12758 ACGTGTAGGATTAGGATCAGAACCCAGGCTCTTTGTCCTTTGGGCTTGTGGAGAA 12817
QY 705 ----- 705
Db 12818 CAGTGCATCCTTCAGAACAGTGCAATCTTAAGCAGCTCCTATGGCTCATGGTATCCCCAG 12877
QY 705 ----- 705
Db 12878 AGTCTGGGAGGACCTCAAACTCCTCATGCTGGTGTGTGTCCTCTCTCACA 12937
QY 706 GlyGlyArgLeuProCysProGluLeuCysProAspAlaValPheArgLeuMetGluGln 725
Db 12938 GGGGGCGCTGCGCTGCCAGAGCTGTCTGATCCGCTTCAGGCTCATGGAGCAG 12997
QY 726 CysTrpAlaTyrGluProGlyGlnArgProSerPheThrIleTyrGlnGluLeuGln 745
Db 12998 TGCTGGGCTATAGAGCTGGCAGCGGCCAGCTTCAGCACCATTCTACAGGAGCTGCAG 13057
QY 746 SerIleArgLysArgHisArg 752
Db 13058 AGCATCCGAAAGCGCATCGG 13078

RESULT 5
US-08-306-691B-35
; Sequence 35, Application US/08306691B
; Patent No. 5734039
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Skorski, Tomasz
; TITLE OF INVENTION: ANTISENSE
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorigna & Monaco, P.C.
; STREET: Two Penn Center, Suite 1800
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,691B
; FILING DATE: September 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
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ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: No. 5734039e
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 3623 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-306-691B-35

Alignment Scores:
Pred. No.: 9.85e-51 Length: 3623
Score: 624.50 Matches: 138
Percent Similarity: 53.79% Conservative: 68
Best Local Similarity: 36.03% Mismatches: 128
Query Match: 16.10% Indels: 49
DB: 1 Gaps: 10

US-10-660-763-2 (1-752) x US-08-306-691B-35 (1-3623)
QY 405 AspArgHisSerThrSerSerSerGluGlnGluArgGluGlyGlyArgThrProThrLeu 424
Db 514 GAGAAACACTCTCGTACCATGGGCTGTGTCCGCAATGCCGTGATATCCG----- 567
QY 425 GluLeuLeuSerHisIleSerGlyLePheArgProLysPheSer----- 440
Db 568 -----CTGACGACGGGATCAATGGGAGCTTCTTGGTGGTGAGATGAGAGCAGTCTCT 621
QY 440 ----- 440
Db 622 ACCCAGAGTCCATCTCGCTGAGATACGAGGGGTGTACCATTTACAGGATCAACACT 681
QY 441 -----AsnLeuTyrArgLeuGluGlyGlyGlyPheProSerIleProLeuLeu 456
Db 682 GCTTCTGTGTCAGCTCTACGTCTCTCCGAGAGCCGCTTCAACACCCCTGGCCAGTTG 741
QY 457 IleAspHis-----LeuLeuSerThr---GlnGlnProLeuThr 468
Db 742 GTTCATCATCTTCAACGGTGGCCGCGGCTCATCACCAGCTCCATTATCCAGCCCA 801
QY 469 LysLysSerGlyValValLeuHisArgAlaValProLys---AspLysTrpValLeuAen 487
Db 802 AAGCGCAACAAGCCCACTGTCTATGTGTGTCTCCCACTACGACAAGTGGGAGATGGAA 861
QY 488 HisGluAspLeuValLeuGlyGluGlnIleGlyArgGlyAsnPhelGlyValPheSer 507
Db 862 CGCAGCGACATCACCATGAAGCAGCAGCTGGGGGGGCGGAGTACGGGAGGTGTACGAG 921
QY 508 GlyArgLeuArgAlaAspAsnThrLeuValAlaValLysSerCysArgGlu---ThrLeu 526
Db 922 GCGCTGTGGAGAAATACAGCTGACGGTGGCGGTGAAGACCTTGAAGAGGAGACCATG 981
QY 527 ProProAspLeuLysAlaLysPheLeuGlnGluAlaArgIleLeuLysGlnTyrSerHis 546
Db 982 GAGGTGGAA-----GAGTTCTTGAAGAAGCTGCAGTGCATGAAGAGATCAAAACAC 1032
QY 547 ProAsnIleValArgLeuIleGlyValCysThrGlnLysGlnProIleTyrIleValMet 566
Db 1033 CCTAACCTAGTCAGCTCTCTGGGGTCTGCACCCGGGAGCCCGCTTATATCATCACT 1092
QY 567 GluLeuValGlnGlyGlyAspPheLeuThrPheLeuArgThrGluGlyAlaArgLeuArg 586
Db 1093 GAGTTTCATGACCTACGGGAACCTCTCTGGACTACCTGAGG---GAGTGCACACGGCAGGAG 1149
QY 587 ValLys-----ThrLeuLeuGlnMetValGlyAspAlaAlaAlaGlyMetGluTyrLeu 604
Db 1150 GTGAACGCCGCTGGTGTGTGTATATGGCCACTCAGATCTCGTCAGCCATGGAGTACCTA 1209
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Qy	605	GluSerLysCysCysIleHisArgAspLeuAlaAlaArgAsnCysLeuValThrGluLys	624
Db	1210	GAGAAAGAAAACATTCATCCACAGAGATCTTGCTGCCGAAACTGCCTGGTAGGGGAGAAC	1269
Qy	625	AsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAlaAspGlyValTyrAla	644
Db	1270	CAC TTG GTG AAG GTAG TCG ATTTTGGCTGTAGCAGGTTGATGCAGGGGACACCTACACA	1329
Qy	645	AlaSerGlyGlyLeuArgGlnValProValLysTrpThrAlaProGluAlaLeuAsnTyr	664
Db	1330	GCCCATGCTGGAGCCAG--TTCCCATCAATGGACTGCACCCGAGAGGCTGGCCTAC	1386
Qy	665	GlyArgTyrSerSerGluSerAspValTrpSerPheGlyIleLeuLeuTrpGluThrPhe	684
Db	1387	AACAAGTTCATCAAGTCGACGCTCTGGGCATTTGGAGTATTGCTTTGGGAAATTGCT	1446
Qy	685	SerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThrArgGluPheValGlu	704
Db	1447	ACCTATGGCATGTCCTCCCTTACC CGGGAATTGACCGTTCCAGGTGTATGAGCTCTAGAG	1506
Qy	705	LysGlyGlyArgLeuProCysProGluLeuCysProAspAlaValPheArgLeuMetGlu	724
Db	1507	AAGACTACGCGATGAAGCCCAAGAGGTGCCAGAGAGGTCTATGAACTCATCGGA	1566
Qy	725	GlnCysTrpAlaTyrGluProGlyGlnArgProSerPheSerThrIleTyrGlnGluLeu	744
Db	1567	GCATGTTGGCAGTGGGAATCCCTCTGACCGGCCCTCCCTTGTGTAATCCACCAACGCTTT	1626

RESULT 6
US-09-949-016-927
; Sequence 927, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 927
; LENGTH: 5434
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-927

Alignment Scores:	
Pred. No.:	1.87e-50
Score:	624.50
Length:	5434
Matches:	138
Percent Similarity:	53.79%
Conservative:	68
Best Local Similarity:	36.03%
Mismatches:	128
Query Match:	49
Indels:	10
DB:	4
Gaps:	10

US-10-660-763-2 (1-752) x US-09-949-016-927 (1-5434)

Qy	405 AspArgHisSerThrSerSerSerGluGlnGluArgGluGlyGlyArgThrProThrLeu	424
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Db	421 GAGAAACACTCTGTATCCATGGGCCTGTGCCCGCAATGCCGTGAGTATCCG	474
Qy	425 GluIleLeuLysSerHisIlesSerGlyIlePheArqProLysPheSer-	440

Db	475	-----CTGAGCAGCGGGATCAATGGCAGCTTCTTGTCGTCGAGAGTCAGAGCTCCT	528
Qy	440	-----	440
Db	529	AGCCAGAGTCCATCTCGCTGAGATACGAAGGAGGGTGTACCATTTACAGGATCAACACT	588
Qy	441	-----AsnLeuTyArgLeuGluGlyGluGlyPheProSerIleProLeuLeu	456
Db	589	GCTTCTGATGGCAAGCTCTAGCTCTCTCCGAGAGCCGCTTCAACACACCCCTGGCCGAGTTG	648
Qy	457	IleAspHis-----LeuLeuSerThr-----GlnGlnProLeuThr	468
Db	649	GTTCATCATCATTTCAACGGTGGCCGAGCGGCTCATCACACGCTCCATTTATCCAGCCCA	708
Qy	469	LySLyAserGlyValValLeuHisArgAlaValProLys---AspLysTrpValLeuAsn	487
Db	709	AAGGCCAACAGCCCACTGCTATGTGTGTCCCCCACTACGACAAAGTGGGAGATGGAA	768
Qy	488	HisGluAspLeuValLeuGlyGluGlnIleGlyArgGlyAsnPheGlyGluValPheSer	507
Db	769	CGCACGGACATCACCATGAAGCACAAAGCTGGCGGGCCAGTAGTACGGGAGGTGTACGAG	828
Qy	508	GlyArgLeuArgAlaAspAsnThrLeuValAlaValLysSerCysArgGlu---ThrLeu	526
Db	829	GGCGTGGGAAGAAATACAGCTGACGGTGGCCGTGAAGACCTTTGAAGGAGGACACATG	888
Qy	527	ProProAspLeuLysAlaLysPheLeuGlnGluAlaArgIleLeuLysGlnTySerHis	546
Db	889	GAGGTGGAA-----GAGTCTTTGAAGAAGCTGCAGTCATGAAGAGATCAACAC	939
Qy	547	ProAsnIleValArgLeuIleGlyValCysThrGlnLysGlnProIleTyIleValMet	566
Db	940	CCTAACCTAGTCAGCTCTCTGGGGTCTGCACCGGGAGCCCGCTTCTATATCATCACT	999
Qy	567	GluLeuValGlnGlyGlyAspPheLeuThrPheLeuArgThrGluGlyAlaArgLeuArg	586
Db	1000	GAGTTGATGACCTACGGGAACTCTCTGGACTACTCTGAGG-----GAGTGCAACCGCAGGAG	1056
Qy	587	ValLys-----ThrLeuLeuGlnMetValGlyAspAlaAlaAlaGlyMetGluTyIleu	604
Db	1057	GTGAACCGCGTGTGTGTGTATGTCATGGCCACTCAGATCTCGTCAGCCATGGAGTACCTA	1116
Qy	605	GluSerLysCysCysIleHisArgAspLeuAlaAlaArgAsnCysLeuValThrGluLys	624
Db	1117	GAGAAGAAAACTTCATCCACAGAGATCTTGTCGCCGAAACTGCTGTGAGGGGAGAAC	1176
Qy	625	AsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAlaAspGlyValTyAla	644
Db	1177	CACTTGGTGAAGTACTGATTTTGGCCTGACAGAGTTGATCACAGGGGACACCTACACA	1236
Qy	645	AlaSerGlyGlyLeuArgGlnValProValLysTrpThrAlaProGluAlaLeuAsnTyI	664
Db	1237	GCCCATGCTGGAGCCCAAG---TTCCCCATCAATGGACTGCACCCGAGAGCCCTGCGCTAC	1293
Qy	665	GlyArgTy-SerSerGluSerAspValTrpSerPheGlyIleLeuLeuTrpGluThrPhe	684
Db	1294	AACAAGTCTCCATCAAGTCCGACGCTGGGCAATTTGGAGTATTCGTTTGGGAATTCGT	1353
Qy	685	SerLeuGlyAlaSerProTyIleProAsnLeuSerAsnGlnGlnThrArgGluPheValGlu	704
Db	1354	ACCTATGGCATGTCCTTACCCGGGAATTGACCGTTCCAGGTGTATGAGCTGTAGAG	1413
Qy	705	LysGlyGlyArgLeuProCysProGluLeuCysProAspAlaValPheArgLeuMetGlu	724
Db	1414	AAGGACTACCGCATGAAGCGCCCAAGAGGCTGCCAGAGAAAGTCTATGAACCTATGCGA	1473
Qy	725	GlnCysTrpAlaTyArgProGlyGlnArgProSerPheSerThrIleTyIleGlnGluLeu	744
Db	1474	GCATTTGGCAGTGGAAATCCCTCTGACCGGCCCTCTTCTTGCTGAATTCACCAAGCCCTT	1533
Qy	745	GlnSerile 747	

Db 1534 GAAACAATG 1542

RESULT 7

US-09-949-016-3759

; Sequence 3759, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3759

; LENGTH: 5763

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-3759

Alignment Scores:

Pred. No.:	3 61e-50	Length:	5763
Score:	622.00	Matches:	158
Percent Similarity:	48.67%	Conservative:	79
Best Local Similarity:	32.44%	Mismatches:	136
Query Match:	16.04%	Indels:	114
DB:	4	Gaps:	17

US-10-660-763-2 (1-752) x US-09-949-016-3759 (1-5763)

Qy	360	LeuGlnGluAlaLeu		-----GlnGlyLeuGlnVal	369
Db	454	CTGGAAGAAGCCCTTACGCGCCAGTAGCATCTGACTTTGAGCCTCAGGGTCTCAGGTGAA			513
Qy	370	AlaLeuCysSerGlnAlaLysLeuGlnAlaGlnGlnGluLeuLeuGlnThrIysLeuGlu		-----	389
Db	514	GCC-----GCTCGTTGGAACCTCAAGAAACCTTCTC		-----	546
Qy	390	HisLeuGlyProGlyGluProProProValLeuLeuLeuGln		-----	403
Db	547	---GCTGGACCCAGTGAAATGACCACCTTTTCGTTGCACCTGTATGATTTTGTGGCC		-----	603
Qy	404	-----AspAsp		-----Arg	406
Db	604	AGTGGAGATAACACTCTAAGCATAACTAAAGGTGAAGAGCTCGGGTCTTAGGCTATAAT		-----	663
Qy	407	HisSerThrSerSerSerGluGlnGluArgGluGlyArg		-----	420
Db	664	CACAATGGGAATGGTGTGAAGCCAAACCAAAATGGCCAGGGCTGGGTCCCAAGCAAC		-----	723
Qy	421	-----ThrPro-----ThrLeuGlu		-----	425
Db	724	TATATCAGCCAGTCAACAGTCTGGAGAAAACACTCTCTGGTACCATGGGCTGTGTCGCCG		-----	783
Qy	426	-----IleLeuLysSerHisIleSerGlyIlePheArgProLysPheSer		-----	440
Db	784	AATGCGGTGATATCTCTGAGCAGCGGATCAATGGCAGCTTCTTGGTGGGTGAGAT		-----	843
Qy	440	-----		-----	440
Db	844	GAGAGCAGTCTGGCCAGAGGTCCATCTCGCTGAGATACGAAGGAGGGGTGACCATTAC		-----	903
Qy	441	-----AsnLeuTyrArgLeuGluGlyPheProSer		-----	452
Db	904	AGGATCAACACTGCTTCTGTATGGCAAGCTCTACGTTCTCTCCCGAGAGCCGCTTCAACACC		-----	963

Wed Aug 10 16:17:25 2005

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Db      1425 CGAAGAGCTG 1434
      : : : : : : : : : :
RESULT 9
US-09-741-154-1
; Sequence 1, Application US/09741154
; Patent No. 6437110
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen M. et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01061
; CURRENT APPLICATION NUMBER: US/09/741,154
; CURRENT FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Human
US-09-741-154-1

Alignment Scores:
Pred. No.:      1,41e-49      Length:      1713
Score:          607.50      Matches:      156
Percent Similarity: 51.23%      Conservative: 53
Best Local Similarity: 38.24%      Mismatches: 115
Query Match:      15.66%      Indels:      84
DB:                3      Gaps:        15

US-10-660-763-2 (1-752) x US-09-741-154-1 (1-1713)
Qy      378 GlnAlaGlnGlnLeuLeuGlnThrLysLeuGlnHisLeuGlyProGly----- 394
Db      288 CGTGTGACGACGAGCTTCTGCTGTTCCACGGGAAGATCTCGGGCCAGGAGGCTGTCCA 347
Qy      395 -----GluProPro-----GluProPro----- 397
Db      348 CGAGCTGCAGCTCCCGAGGATGGCTGTTCTGCTGGGGAGTCCGGCGCCACCCCGG 407
Qy      398 -----ProValLeuLeuGlnAspAspArgHisSerSerSerSerGluGln 414
Db      408 CGACTACGTCCTGTCGCGAGCTTTGGCGCGGAGCTCATCCACTACCGCGTGTGCAACCG 467
Qy      415 GluArgGluGlyGlyArgThrPro-ThrLeuGlnLeuLysSerHisLeuGly11 434
Db      468 CGA-----CGGCCACCTCACATCGAT-----GAGGCGGT 497
Qy      434 ePheArgProLysPheSerAsnLeuTyArgLeuGluGlyGluGlyPheProSerIlePr 454
Db      498 GTTC-----TTCTGCACTCATGGAC----- 519
Qy      454 oLeuLeuLeuAspHisLeuLeuSerThrGlnGlnProLeuThrLysSerGlyValva 474
Db      520 ----ATGGTGGAGCAT-----TACAGCAAGGACAAGGGGGCTAT 554
Qy      474 lLeuHisArgAlaVal---ProLysAspLys----- 483
Db      555 GTGCACCAAGCTGGTAGACCAAGCGGAAACACGGGACCAAGTCGGCGGAGGAGAGCT 614
Qy      484 -----TrpValLeuAsnHisGluAspLeuValLeuGlyGluGlnIleGlyAr 499
Db      615 GGCCAGGCGGGCTGTTACTGAACCTGCAGCATTTGACATTTGGGAGCAGACATCGGAGA 674
Qy      499 gGlyAsnPheGlyGluValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlava 519
Db      675 GGAGAGATTTGGAGCTGCTCTCGAGGGTGAGTACCTCGGGGCAAAAG-----GTGCCGT 728
Qy      519 lLysSerCysArgGluThrLeuProProAspLeuLysAlaLys---PheLeuGlnGluAl 538
Db      729 GAAGAAT-----ATCAAGTGTGATGTGACAGCCAGGCGCTTCTCTGGACGAGAC 776
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728  CCTGTGCGTGAGCTTTGGCCGCGCATCCAC-----
441  nLeuTyrArg---LeuGluGlyGluGlyPheProSerIle-----ProLeuLeuIleAs 458
762  ---TACCCTGCTGCTGACCGCGGCGGCGCCTCACATCGATGAGGCGGTCTTCTCTG 817
458  pHisLeuLeuSerThrGlnGlnProLeuThrIlySerGlyValValLeuHisArgAl 478
818  CAACCTCATGGACATGTTGGAGCATATACAGCAAGCAAGGCGGTATCTCTGCAACAGCT 877
478  aVal---ProLysAspLys-----
878  GGTGAGACCAAGCGGAAACACGCGGACCAAGTCGCGCGGAGGAGTGCGCCAGGCGGG 937
484  -TrpValLeuAenHisGluAspLeuValLeuGlyGluGlnIleGlyArgGlyAanPheGl 503
938  CTGGTTACTGAACCTCGACATTTGACATTTGGAGCACAGATCGGAGAGGAGAGTTTGG 997
503  yGluValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaValIlySerCys 523
998  AGCTGTCTCTGAGGCTGAGTACCTGGGGCAAAAG-----GTGGCGGTGAAGAAT- 1046
523  gGluThrLeuProProAspLeuIlySAlaLys---PheLeuGlnGluAlaArgIleLeu 542
1047  -----ATCAAGTGTGATGTGACACCCAGGCTTCTCTGGCGGTGATCTCTGCAC- 1099
542  sGlnTyrSerHisProAsnIleValArgLeuIleGlyValCysThrGlnLysGlnProI 562
1100  GAAGATCAACACAGAGNACCTGTGTCTCTCTGGCGGTGATCTCTGCAC- 1156
562  eTyrIleValMetGluLeuValGlnGlyGlyAspPheLeuThrPheLeuArgThrGluGl 582
1157  GTACATTTGTATGAGCAGCAGTGTGAGCAAGGCAACCTGGTGAACCTTTCTCGGACCCG 1216
582  y---AlaArgLeuArgValIlyThrLeuLeuGlnMetValGlyAspAlaAlaIle 601
1217  TCGAGCCCCCTGTGAACACCCGCTCAGCTCTCTGAGTTTCTCTGCACGTGGCGGAGGCAT 1276
601  tGluTyrLeuGluSerLysCysIleHisArgAspLeuAlaAlaArgAsnCysLeuVal 621
1277  GGAGTACCTGAGAGCAAGAGCTTGTGCACCGCGACCTGGCGCGCGCGCAACATCTCTGT 1336
621  lThrGluLysAsnValLeuIlySerAspPheGlyMetSerArgGluGluAlaAspGl 641
1337  CTCAGAGACCTGTGTGGCAAGGTACGAGCTTTGGCTCGCCCAAGCCGCGGAGGAG 1396
641  yValTyrAlaAlaSerGlyGlyLeuArgGlnValProValIlyTrpThrAlaProGluAl 661
1397  GCTAGACTCAAG-----CGCTGCTCGCTCAAGTGGAGCGCGCGCGCGG 1441
661  aLeuAsnTyrGlyArgTyrSerSerGluSerAspValTrpSerPheGlyIleLeuLeuTr 681
1442  TCTCAACACCGGAAGTTTACACAGCAAGTCTGAGTGTCTGGAGTTTGGGGTGTCTCTCT 1501
681  pGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGlnGlnThrArgGl 701
1502  GGAGTCTTCTCATATGAGCGGCTCCGTACCTTAAATGTCACTGCTAAAGAGGAGTCCGA 1561
701  uPheValGluLysGlyArgLeuProCysProGluLeuCysProAspAlaValPheAr 721
1562  GGCGGTGGAGAGGGGTACCGCATGGAACCCCGGAGGCTGTCTCAGCGCCCGTGCACGT 1621
721  gLeuMetGluGlnCysTrpAlaTyrGluProGlyGlnArgProSerPheSerThrIleTy 741
1622  CCTCATGAGCAGCTGTCTGGAGGCGAGACCCCGCGCGCGCCACCTTTCGCAACCTGGC 1681
741  rGlnGluLeu 744
1682  CGAAGAGCTG 1691

RESULT 12
US-08-232-545-1
; Sequence 1, Application US/08232545

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Qy 621 lThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGluGluAlaAspG1 641
Db 1337 CTCAGAGGACCTGTCGCAAGGTCAGCGACTTTGGCTGGCCAAAGCCGAGCGGAAGGG 1396
Qy 641 yValTyAlaAlaSerGlyGlyLeuArgGlnValProValIysTrpThrAlaProGluAl 661
Db 1397 GCTAGACTCAAGC-----CGGCTGCCGTCAGGTGGACGGCGCCGAGGC 1441
Qy 661 aLeuAsnTyGlyArgTySerSerGluSerAspValTrpSerPheGlyIleLeuLeuTr 681
Db 1442 TCTCAACACGGGAAGTTCACCAAGTCGATGCTCGAGTTTGGGTGCTGCTCTG 1501
Qy 681 pGluThrPheSerLeuGlyAlaSerProTyProAsnLeuSerAsnGlnGlnThrArgG1 701
Db 1502 GGAGGTCTCTCATATGACGGGCTCGTACCTTAAATGTCACTGAAAGAGGTGTGCGA 1561
Qy 701 uPheValGluLysGlyGlyArgLeuProCysProGluLeuCysProAspAlaValPheAr 721
Db 1562 GGCGGTGGAGAAGGGGTACCGCATGGAAACCCCGAGGGGCTGTCCAGGCCCGTGCACTG 1621
Qy 721 gLeuMetGluGlnCysTrpAlaTyGluProGlyGlnArgProSerPheSerThrIleTy 741
Db 1622 CCTCATGAGCAGCTGCTGGAGGAGGAGAGCCGCGCCGCGCCACCTTTCGCCAACTGGC 1681
Qy 741 rGlnGluLeu 744
Db 1682 CGAGAAGCTG 1691

RESULT 14
US-08-604-989A-9
; Sequence 9, Application US/08604989A
; Patent No. 5834208
; GENERAL INFORMATION:
; APPLICANT: Sakano, S.
; TITLE OF INVENTION: No. 5834208e1 Tyrosine Kinase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/604,989A
; FILING DATE: February 23, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles E. Miller
; REGISTRATION NUMBER: 24,576
; REFERENCE/DOCKET NUMBER: 1920-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1398 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: human
; STRAIN: UT-7
US-08-604-989A-9

Alignment Scores:

Pred. No.: 3,55e-49 Length: 1398
Score: 602.00 Matches: 174
Percent Similarity: 47.93% Conservative: 69
Best Local Similarity: 34.32% Mismatches: 164
Query Match: 15.52% Indels: 101
DB: 2 Gaps: 18

US-10-660-763-2 (1-752) x US-08-604-989A-9 (1-1398)

Qy 267 GlnTyGlySerAlaProAspValProProCysValThrPheAspGluSerLeuLeuGlu 286
Db 5 CAACGAGGCGCTGGCGCCCGGCGCCAG-TGATCACC-----AAATGGCAG 51
Qy 287 GluGlyGluProLeuGluProGlyGluLeuGlnLeuAsnGluLeuThrValGluSerVal 306
Db 52 CACACCGCGCCC--AAGCCAGGGGAGCTG-----78
Qy 307 GlnHisThrLeuThrSerValThrAspGluLeuAlaValAlaThrGluMetValPheArg 326
Db 79 -----GCTTCCGC 87
Qy 327 ArgGlnGluMetValThrGlnLeuGlnGlnLeuArgAsnGluGluGlnAsnThrHis 346
Db 88 AAGGCGAGCTGTGTACCATCTCTGGAGGCC-----TCCGAGAACAGAGCTGG 135
Qy 347 ProArgGluArgValGlnLeuLeuGlyLysArgGlnValLeuGlnGluAlaLeuGlnGly 366
Db 136 TACCGGCTCAAGCACACACAGCTGCACAGAGGGCTGTGGCAGCTGGGGCGCTGCGG 195
Qy 367 LeuGlnValAlaLeuCysSerGlnAlaLysLeuGln-----378
Db 196 GAGCGGAGGCGCTCTCCGACAGACCCCAAGCTCAGCTCAGCTGCTGCTCCAGGGGAAG 255
Qy 379 --AlaGlnGlnGluLeuGlnThrLysLeuGluHisLeuGlyProGlyGluProPro 397
Db 256 ATCTCGGGCAGAGGCTGTCCAG-----CAGCTGAGCTCCCGAGGATGGG 303
Qy 398 ProValLeuLeuGlnAspAspArgHisSerThrSerSerSerGluGlnGluArgGlu 417
Db 304 CTGTTCTGTGGGGAGTCCGCGCCAC-----CCC 336
Qy 418 GlyGlyArgThrProThrLeuGluLysSerHisIleSerGlyIlePheArgPro 437
Db 337 GCGCACTACGTCCTGTGCGTGTGGCTTTGGCGCGAGCTCATCCAC-----381
Qy 438 LysPheSerAsnLeuTyArg---LeuGluGlyGluGlyPheProSerIle-----Pro 454
Db 382 -----TACCGCTGTGTCACCGCAGCGCCACCTCACATCGATGAGGCC 426
Qy 455 LeuLeuIleAspHisLeuLeuSerThrGlnGlnProLeuThrLysLysSerGlyValVal 474
Db 427 GTGTTCTTGCACCTCATGGACATGGTGGACATTCACAGCAAGGACAGGGCGCTATC 486
Qy 475 LeuHisArgAlaVal---ProLysAspLys-----483
Db 487 TGCACCAAGCTGTGTAGACCAAGCAACACCGGACCAAGTCGCGCCGAGGAGGAGCTG 546
Qy 484 -----TrpValLeuAsnHisGluAspLeuValLeuGlyGluGlnIleGlyArg 499
Db 547 GCCAGGGCGGGCTGGTTACTGAACTTCGACATTTGACATTTGGGAGCAGATCGGAGAG 606
Qy 500 GlyAsnPheGlyGluValPheSerGlyArgLeuArgAlaAspAsnThrLeuValAlaVal 519
Db 607 GGAGAGTTTGGAGCTGTCTGTCAGGGGTGAGTACTTGGGGCAAG-----GTGGCGCTG 660
Qy 520 LysSerCysArgGluThrLeuProProAspLeuLysAlaLys---PheLeuGlnGluAla 538
Db 661 AAGAAAT-----ATCAAGTGTGTGTGACAGCCCGAGCCCTTCTCTGGACGAGACG 708
Qy 539 ArgIleLeuLysGlnTySerHisProAsnIleValArgLeuIleGlyValCysThrGln 558
Db 709 GCGTCATGACGAAGATGCACAGAACCTGTGCTCTCTGGGGCGTATCTCTGCAC 768

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US-10-660-763-2 (1-752) x US-09-949-016-5357 (1-2572)
QY 327 ArgGlnGluMetValThrGlnLeuGlnGlnLeuAraGlnGluGlu----- 343
Db 409 CGGACGGCTGGGTGCTGCGCTTAAAGAAAGAAACGAGGATAATAACAGATTGGTGCT 468
QY 344 AsnThrHisProArgGluArgValGlnLeuLeuGlyLysArgGlnValLeuGlnGluAla 363
Db 469 AATATATCACTCT-----AATTTCTGGATGGATGGGAGTG--GAGGTGCTGTTCTCAGCT 521
QY 364 LeuGlnGlyLeuGlnValAlaLeuCysSerGlnAlaLysLeuGlnAlaGlnGlnGlu--- 382
Db 522 GG-AGAAGCTTGCAACAGGCTGTGCCCAATATATCAACCAAGAAATGCTTCAAAGAAGC 580
QY 383 -----LeuLeuGlnThrLysLeuGluHisLeuGly----- 392
Db 581 CTCTTCCTCTACTCTCTGAAGACACACAGCGGACCACTTTGGGAACCTGAAGAACTGTGG 640
QY 393 -----ProGlyGluProProValLeuLeuLeuGlnAsp 404
Db 641 TCATTGCTTATATGACTACCAACCAAT-GATCCTCAGAACTCGCACTGCGGCGCAAC 699
QY 405 AspArgHisSer---ThrSerSerSerGlu-----GlnGluArgGlu 417
Db 700 GAAGAGTACTGCTGCTGGACAGTTCTGAGATTCACTGGTGGAGAGTCCAGGACAGGAAT 759
QY 418 Gly----- 419
Db 760 GGGTGTACATAAGAGTATCAGCGGAGACAAAGCTGAAAAAATCTTTTGGACACAGGC 819
QY 420 ArgThrProThrLeuGluLeuLeuLysSerHisIleSerGlyIlePhe----- 435
Db 820 AAAGAAGGAGGCTTTCATGGTAAAGGATTCAGGAGACTCGAGGAACATACACCGTGTCTGTT 879
QY 435 ----- 435
Db 880 TTCACCAAGGCTGTTGTAAGTGAGAACAAATCCCTGTATTAAGCAATTATCATCAAGGAA 939
QY 436 -----ArgProLysPheSerAsnLeuTyArgLeuGluGlyGluGlyPheProSer 452
Db 940 ACAAAATGACAAATCTCTAAG-----CGATACATATGCTGGCTGAAAGATGATGTTGATTCC 993
QY 453 IleProLeuLeuIleAspHisLeuLeuSerThrGlnGlnProLeuThrLysLysSerGly 472
Db 994 ATCCCTCTCTCATCACTAT----- 1014
QY 473 ValValLeuHisArgAlaValProLysAspLysTyrValLeuAsnHisGluAspLeuVal 492
Db 1015 -----CACCAACATAATGGAGGAGGAAATGGGTGATCGACCCCTCAGAGTCACT 1065
QY 493 LeuGlyGluGlnIleGlyArgGlyAsnPheGlyGluValPheSerGlyArg---LeuArg 511
Db 1066 TTTGTGCAAGAGATTTGGCAGTGGGCAATTTGGTGGTGGTGCATCTGGCTACTGGCTCAAC 1125
QY 512 AlaAspAsnThrLeuValAlaValLysSerCysArgGluThrLeuProAspLeuLys 531
Db 1126 AAGGACAAG-----GTGGCTATCAAAACCATTCGGGAAGGGGCTATGTCAGAA----- 1173
QY 532 AlaLysPheLeuGlnGluAlaArgIleLeuLysGlnTyrSerHisProAsnIleValArg 551
Db 1174 GAGGACTTCATAGAGGAGGCTGAAGTATGATGAAACTCTCTCATCCCAAACTGGTGCAG 1233
QY 552 LeuIleGlyValCysThrGlnLysGlnProIleTyrIleValMetGluLeuValGlnGly 571
Db 1234 CTGTATGGGGTGTGCTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1293
QY 572 GlyAspPheLeuThrPheLeuArgThrGluGlyAlaArgLeuArgValLysThrLeuLeu 591
Db 1294 GGCTGCTGTCAGATTATCTACGACCCCGGGGAGCTTTTCTGCAGAGACCCCTGCTG 1353
QY 592 GlnMetValGlyAspAlaAlaAlaGlyMetGluTyrLeuGluSerLysCysIleHis 611
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559 LysGlnProIleTyrIleValMetGluLeuValGlnGlyGlyAspPheLeuThrPheLeu 578
Db 769 ---CAGGGCTGTACATTTGATGAGCAGCGTGAACAGGCAACCTGTTGACTTTCTG 825
QY 579 ArgThrGluGly---AlaArgLeuArgValLysThrLeuLeuGlnMetValGlyAspAla 597
Db 826 CGACCCCGGGTGCAGCCCTCGTGAACACCGCTCAGCTCTGCTGCTGCTGCTGCTGCTG 885
QY 598 AlaAlaGlyMetGluTyrLeuGlnSerLysCysIleHisArgAspLeuAlaAlaArg 617
Db 886 GCGGAGGCTGAGTACCTCGGAGACCAAGAGCTTTGTCACCGGACCTGCGCCCGCCGCG 945
QY 618 AsnCysLeuValThrGluLysAsnValLeuLysIleSerAspPheGlyMetSerArgGlu 637
Db 946 AACATCTGCTCTCAGGAGGACCTGTTGGCCAGGTCAGCGACTTTGGCTGCGCCAAAGCC 1005
QY 638 GluAlaAspGlyValTyrAlaAlaSerGlyGlyLeuArgGlnValProValLysTrpThr 657
Db 1006 GAGCGGAAGGGCTAGACTCAAGC-----CGGCTGCGCCGCTCAAGTGGACG 1050
QY 658 AlaProGluAlaLeuAsnTyrGlyArgTyrSerSerGluSerAspValTrpSerPheGly 677
Db 1051 GCGCCCGGAGGCTCTCAAAACACGGGAAGTTCACCAAGCAAGTCTGCTGAGTCTTTGGG 1110
QY 678 IleLeuLeuTrpGluThrPheSerLeuGlyAlaSerProTyrProAsnLeuSerAsnGln 697
Db 1111 GTGCTGCTCTGGAGGCTCTTCATATGAGGAGGCTCGCTACCTAAATGTCACTGAAA 1170
QY 698 GlnThrArgGluPheValGluLysGlyGlyArgLeuProCysProGluLeuCysProAsp 717
Db 1171 GAGGTGTCGGAGGCGCTGGAAGAGGGTACCGCATGAAACCCCGAGGCTGTCCAGGC 1230
QY 718 AlaValPheArgLeuMetGluGlnCysTrpAlaTyrGluProGlyGlnArgProSerPhe 737
Db 1231 CCCGTGCACCTCTCATGACGAGCTGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1290
QY 738 SerThrIleTyrGlnGluLeu 744
Db 1291 CGCAAACTGGCGGAGAGCTG 1311
RESULT 15
US-09-949-016-5357
; Sequence 5357, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5357
; LENGTH: 2572
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5357
Alignment Scores:
Pred. No.: 2,05e-48 Length: 2572
Score: 598.50 Matches: 165
Percent Similarity: 46.98% Conservative: 68
Best Local Similarity: 33.27% Mismatches: 163
Query Match: 15.43% Indels: 103
DB: 4 Gaps: 14
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Db      1354  GGCATGTGCTGGGATGTGTGAGGGCATGGCCCTACTGGAGAGGGCATGTGTCTATCCAC 1413
Qy      612  ArgAspLeuAlaAlaArgAsnCysLeuValThrGluLysAsnValLeuLysIleSerAsp 631
Db      1414  AGACATTTGGCTGCCAGAAATTGTTGGTGGAGAAAACCAAGTCATCAAGGTGCTCTGAC 1473
Qy      632  PheGlyMetSerArgGluGluAlaAspGlyValTyrAlaAlaSerGlyLeuArgGln 651
Db      1474  TTTGGGATGACAAGGTTTCGTTCGTGATGATCAGTACACCAAGTTCCACAGGCACCAAA--- 1530
Qy      652  ValProValLysTrpThrAlaProGluAlaLeuAsnTyrGlyArgTyrSerSerGluSer 671
Db      1531  TTCCCGGTGAAGTGGGCATCCCCAGAGGTTTCTTTTCAGTCGCTATAGCAGCAAGTCC 1590
Qy      672  AspValTrpSerPheGlyIleLeuLeuTrpGluThrPheSerLeuGlyAlaSerProTyr 691
Db      1591  GATGTGTGGTCATTTGTGTGCTGATGTGGGAAGTTTTTCAGTGAAGGCAAAATCCCGTAT 1650
Qy      692  ProAsnLeuSerAsnGlnGlnThrArgGluPheValGluLysGlyArgLeuProCys 711
Db      1651  GAAACCCGAAAGCAACTCAGAGGTGGTGGAAAGACATCAGTACCGGATTTTCGGTTGTACAAG 1710
Qy      712  ProGluLeuCysProAspAlaValPheArgLeuMetGluGlnCysTrpAlaTyrGluPro 731
Db      1711  CCCCGGTGGCTCCACACACGCTCTACAGATTATGAATCACTCTCTGGAAGAGAGACCA 1770
Qy      732  GlyGlnArgProSerPheSerThrIleTyrGlnGluLeuGlnSerIle 747
Db      1771  GAAGATCGGCCAGCCTTCTCCAGACTGCTGCGTCAACTGGCTGAAATT 1818
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Search completed: August 10, 2005, 10:21:54
Job time : 520 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	3879	100.0	752	13	US-10-003-295-2	Sequence 2, Appli
2	3879	100.0	752	15	US-10-660-763-2	Sequence 2, Appli
3	3834	98.8	822	13	US-10-003-295-4	Sequence 4, Appli
4	3834	98.8	822	15	US-10-660-763-4	Sequence 4, Appli
5	3620	93.3	820	17	US-10-732-923-13687	Sequence 13687, A
6	3620	93.3	820	17	US-10-732-923-13687	Sequence 13687, A
7	2635	67.9	824	17	US-10-732-923-13665	Sequence 13688, A
8	2571	66.3	898	17	US-10-732-923-13481	Sequence 13665, A
9	2570	66.3	873	17	US-10-732-923-13482	Sequence 13481, A
10	2561	66.0	873	17	US-10-732-923-13480	Sequence 13482, A
11	2561	66.0	1182	17	US-10-732-923-13479	Sequence 13480, A
12	2561	66.0	1182	17	US-10-732-923-13479	Sequence 13479, A

Qy	1	MGFSSELCSPOQGHVLIQQOQAEALRLLEGMRKXMAQRVKSDEYAGLLHHMSLQDSGGQS	60
Db	1	MGFSSELCSPOQGHVLIQQOQAEALRLLEGMRKXMAQRVKSDEYAGLLHHMSLQDSGGQS	60
Qy	61	RAISPDSPISQSWAEITTSQTEGLRLLRQHAEDLNSGPLSKLSLIRERQQLRKTYSEQW	120
Db	61	RAISPDSPISQSWAEITTSQTEGLRLLRQHAEDLNSGPLSKLSLIRERQQLRKTYSEQW	120
Qy	121	QQLQBELTHTHSQDIEKLKSOYRALARLSAQAKRYQEASKQDKORDKAKDKTVRSIWLKLF	180

ORGANISM: HOMO SAPIENS
US-10-003-295-2

Local Similarity 100.0%, Ident. No. 2122,
 Matches 752: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Db	121	QQLQOELTKTHSODIEKLKSYRALARDSAQAKRYQEASKDKORDKAKDKYVRSWKLF	180
Qy	181	AHNRYVLGVRAAQLHHQHLLPGLLRSQDLHEEMACILKEILOEYLEISSLVQDE	240
Db	181	AHNRYVLGVRAAQLHHQHLLPGLLRSQDLHEEMACILKEILOEYLEISSLVQDE	240
Qy	241	VVAIHREMAAAARIIOPEAEYQGFRLQYGSAPDVPFVTFDESLLSEGEPLPGELOLNE	300
Db	241	VVAIHREMAAAARIIOPEAEYQGFRLQYGSAPDVPFVTFDESLLSEGEPLPGELOLNE	300
Qy	301	LTVESVOHTLTSVTDELAVATEMVFRRQEMVTOLQOELNEEENTHPRERVOLLKGRVL	360
Db	301	LTVESVOHTLTSVTDELAVATEMVFRRQEMVTOLQOELNEEENTHPRERVOLLKGRVL	360
Qy	361	QEALQGLQVALCSOAKLOAQOELLQTKLEHLGEGEPVPLLLQDDRHSTSSSEQEREGGR	420
Db	361	QEALQGLQVALCSOAKLOAQOELLQTKLEHLGEGEPVPLLLQDDRHSTSSSEQEREGGR	420
Qy	421	TPTLEILKSHISGIFRPFKSNLYRLEGEPPSPILLIDHLLSTQOPLTKKSGVVLHRAVP	480
Db	421	TPTLEILKSHISGIFRPFKSNLYRLEGEPPSPILLIDHLLSTQOPLTKKSGVVLHRAVP	480
Qy	481	KDKVNLHEDLVLGEQIGRNGFVFSGRRLADNTLVAVKSCRETLPPDLKAKFLQEAR	540
Db	481	KDKVNLHEDLVLGEQIGRNGFVFSGRRLADNTLVAVKSCRETLPPDLKAKFLQEAR	540
Qy	541	LKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDPLFLRTEGARLRVKTLLQMWGDAAG	600
Db	541	LKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDPLFLRTEGARLRVKTLLQMWGDAAG	600
Qy	601	MEYLESKCIHRDLAARNCLVTEKNVLSIDFGMSREEDGVYAASGGLRQVPVKWTAPE	660
Db	601	MEYLESKCIHRDLAARNCLVTEKNVLSIDFGMSREEDGVYAASGGLRQVPVKWTAPE	660
Qy	661	ALNYGRYSESDVWSFGILLMETFSLGASPPNLSNQOTREFVEKGGRLPCPELCPDAVF	720
Db	661	ALNYGRYSESDVWSFGILLMETFSLGASPPNLSNQOTREFVEKGGRLPCPELCPDAVF	720
Qy	721	RLMEQCWAYEPQRPSPFSSTIYQELQSIRKRRH	752
Db	721	RLMEQCWAYEPQRPSPFSSTIYQELQSIRKRRH	752
RESULT 2			
US-10-660-763-2			
; Sequence 2, Application US/10660763			
; Publication No. US20040063130A1			
; GENERAL INFORMATION:			
; APPLICANT: GAN, Weiniu et al.			
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC			
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES			
; TITLE OF INVENTION: THEREOF			
; FILE REFERENCE: CL001183DIVI			
; CURRENT APPLICATION NUMBER: US/10/660,763			
; CURRENT FILING DATE: 2003-09-12			
; NUMBER OF SEQ ID NOS: 4			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 2			
; LENGTH: 752			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-660-763-2			
Query Match 100.0%; Score 3879; DB 15; Length 752;			
Best Local Similarity 100.0%; Pred. No. 3.5e-223;			
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	MGFSELCSQGHGVLOQMOEAEIRLLEGKRWKMAQRVKSDREYAGLLHMSIQSGGQS	60
Db	1	MGFSELCSQGHGVLOQMOEAEIRLLEGKRWKMAQRVKSDREYAGLLHMSIQSGGQS	60
Qy	61	RAISPDSPISQSWAEITTSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKYSEQW	120

Db	61	RAISPDSPISQSWAEITTSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKYSEQW	120
Qy	121	QQLQOELTKTHSODIEKLKSOYRALARDSAQAKRYQEASKDKORDKAKDKYVRSWKLF	180
Db	121	QQLQOELTKTHSODIEKLKSOYRALARDSAQAKRYQEASKDKORDKAKDKYVRSWKLF	180
Qy	181	AHNRYVLGVRAAQLHHQHLLPGLLRSQDLHEEMACILKEILOEYLEISSLVQDE	240
Db	181	AHNRYVLGVRAAQLHHQHLLPGLLRSQDLHEEMACILKEILOEYLEISSLVQDE	240
Qy	241	VVAIHREMAAAARIIOPEAEYQGFRLQYGSAPDVPFVTFDESLLSEGEPLPGELOLNE	300
Db	241	VVAIHREMAAAARIIOPEAEYQGFRLQYGSAPDVPFVTFDESLLSEGEPLPGELOLNE	300
Qy	301	LTVESVOHTLTSVTDELAVATEMVFRRQEMVTOLQOELNEEENTHPRERVOLLKGRQVL	360
Db	301	LTVESVOHTLTSVTDELAVATEMVFRRQEMVTOLQOELNEEENTHPRERVOLLKGRQVL	360
Qy	361	QEALQGLQVALCSOAKLOAQOELLQTKLEHLGEGEPVPLLLQDDRHSTSSSEQEREGGR	420
Db	361	QEALQGLQVALCSOAKLOAQOELLQTKLEHLGEGEPVPLLLQDDRHSTSSSEQEREGGR	420
Qy	421	TPTLEILKSHISGIFRPFKSNLYRLEGEPPSPILLIDHLLSTQOPLTKKSGVVLHRAVP	480
Db	421	TPTLEILKSHISGIFRPFKSNLYRLEGEPPSPILLIDHLLSTQOPLTKKSGVVLHRAVP	480
Qy	481	KDKVNLHEDLVLGEQIGRNGFVFSGRRLADNTLVAVKSCRETLPPDLKAKFLQEAR	540
Db	481	KDKVNLHEDLVLGEQIGRNGFVFSGRRLADNTLVAVKSCRETLPPDLKAKFLQEAR	540
Qy	541	LKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDPLFLRTEGARLRVKTLLQMWGDAAG	600
Db	541	LKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDPLFLRTEGARLRVKTLLQMWGDAAG	600
Qy	601	MEYLESKCIHRDLAARNCLVTEKNVLSIDFGMSREEDGVYAASGGLRQVPVKWTAPE	660
Db	601	MEYLESKCIHRDLAARNCLVTEKNVLSIDFGMSREEDGVYAASGGLRQVPVKWTAPE	660
Qy	661	ALNYGRYSESDVWSFGILLMETFSLGASPPNLSNQOTREFVEKGGRLPCPELCPDAVF	720
Db	661	ALNYGRYSESDVWSFGILLMETFSLGASPPNLSNQOTREFVEKGGRLPCPELCPDAVF	720
Qy	721	RLMEQCWAYEPQRPSPFSSTIYQELQSIRKRRH	752
Db	721	RLMEQCWAYEPQRPSPFSSTIYQELQSIRKRRH	752
RESULT 3			
US-10-003-295-4			
; Sequence 4, Application US/10003295			
; Publication No. US20020168741A1			
; GENERAL INFORMATION:			
; APPLICANT: GAN, Weiniu et al.			
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC			
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES			
; TITLE OF INVENTION: THEREOF			
; FILE REFERENCE: CL001183DIV			
; CURRENT APPLICATION NUMBER: US/10/003,295			
; CURRENT FILING DATE: 2001-12-06			
; NUMBER OF SEQ ID NOS: 4			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 4			
; LENGTH: 822			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-003-295-4			
Query Match 98.8%; Score 3834; DB 13; Length 822;			
Best Local Similarity 91.5%; Pred. No. 1.9e-220;			
Matches 752; Conservative 0; Mismatches 0; Indels 70; Gaps 1;			
Qy	1	MGFSELCSQGHGVLOQMOEAEIRLLEGKRWKMAQRVKSDREYAGLLHMSIQSGQS	60

Db 1 MGFSELCSPOGHVLOQMGEAELRLLEGMKMAQVRKSDREYAGLLHHMSLQDSGGQS 60
Qy 61 RAISPDPSPISQSWAEITTSQTEGLSRLLRQHAEDLNSGPKSLSLIRERQQLRKYTSEOW 120
Db 61 RAISPDPSPISQSWAEITTSQTEGLSRLLRQHAEDLNSGPKSLSLIRERQQLRKYTSEOW 120
Qy 121 QOLQELTKTHSDIEKLSQYRALARDSAQAKRYQEASKDKDRDAKAKYVRSWKLF 180
Db 121 QOLQELTKTHSDIEKLSQYRALARDSAQAKRYQEASKDKDRDAKAKYVRSWKLF 180
Qy 181 AHNRYVLGVRAAQLHHQHOLLPGLLRSLQDLHEEMACILKEILQEYLEISLVQDE 240
Db 181 AHNRYVLGVRAAQLHHQHOLLPGLLRSLQDLHEEMACILKEILQEYLEISLVQDE 240
Qy 241 VVAITHREMAAARIQPEAEYQGFRLQYGSAPDVPVPCVTFDESLEEGLPELQELQNE 300
Db 241 VVAITHREMAAARIQPEAEYQGFRLQYGSAPDVPVPCVTFDESLEEGLPELQELQNE 300
Qy 301 LTVESVQHTLTSVTDELAVATEMVFRRQEMVTOLQELRNEEENTHPRERVQLLGRQVL 360
Db 301 LTVESVQHTLTSVTDELAVATEMVFRRQEMVTOLQELRNEEENTHPRERVQLLGRQVL 360
Qy 361 QEALQGLQVALCSQAKLQAQOELLQTKLEHLGPGEPVPLVLLQDDRHSSTSSSEOREGGR 420
Db 361 QEALQGLQVALCSQAKLQAQOELLQTKLEHLGPGEPVPLVLLQDDRHSSTSSSEOREGGR 420
Qy 421 TPTLEILKSHISGIFRPKFS----- 440
Db 421 TPTLEILKSHISGIFRPKFS----- 440
Qy 441 -----NLYRLEGEPSPISPLLIDHLLSTOQPLTKK 470
Db 481 LVRESQKQEVYLSVLDGLPRHFI IQSLDNLVLEGEFPSPISPLLIDHLLSTOQPLTKK 540
Qy 471 SGVVLHRAVPKDKVNLHEDVLVGEQIGRGNFGEVFSGRADNTLVAVKSCRETLPPDL 530
Db 541 SGVVLHRAVPKDKVNLHEDVLVGEQIGRGNFGEVFSGRADNTLVAVKSCRETLPPDL 600
Qy 531 KAKFLQEARILKQYSHNPVRLIGVCTQKQPIYIVMELVQGGDFLTLRTGRLRVKTL 590
Db 601 KAKFLQEARILKQYSHNPVRLIGVCTQKQPIYIVMELVQGGDFLTLRTGRLRVKTL 660
Qy 591 LQVGDAAAGMEYLESKCCIIHRDLAARNCLVTEKNVLIKISDFGMSREADGVYAAAGSLR 650
Db 661 LQVGDAAAGMEYLESKCCIIHRDLAARNCLVTEKNVLIKISDFGMSREADGVYAAAGSLR 720
Qy 651 QVPVKWTAPEALNYGRYSSESDDVMSFGILLWETSLGASYPNLSNOOTREFVEKGRPL 710
Db 721 QVPVKWTAPEALNYGRYSSESDDVMSFGILLWETSLGASYPNLSNOOTREFVEKGRPL 780

RESULT 4

US-10-660-763-4
; Sequence 4, Application US/10660763
; Publication No. US20040063130A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIVII
; CURRENT APPLICATION NUMBER: US/10/660,763
; CURRENT FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 822
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-660-763-4

Query Match 98.8%; Score 3834; DB 15; Length 822;
Best Local Similarity 91.5%; Pred. No. 1.9e-220;
Matches 752; Conservative 0; Mismatches 0; Indels 70; Gaps 1;
Qy 1 MGFSELCSPOGHVLOQMGEAELRLLEGMKMAQVRKSDREYAGLLHHMSLQDSGGQS 60
Db 1 MGFSELCSPOGHVLOQMGEAELRLLEGMKMAQVRKSDREYAGLLHHMSLQDSGGQS 60
Qy 61 RAISPDPSPISQSWAEITTSQTEGLSRLLRQHAEDLNSGPKSLSLIRERQQLRKYTSEOW 120
Db 61 RAISPDPSPISQSWAEITTSQTEGLSRLLRQHAEDLNSGPKSLSLIRERQQLRKYTSEOW 120
Qy 121 QOLQELTKTHSDIEKLSQYRALARDSAQAKRYQEASKDKDRDAKAKYVRSWKLF 180
Db 121 QOLQELTKTHSDIEKLSQYRALARDSAQAKRYQEASKDKDRDAKAKYVRSWKLF 180
Qy 181 AHNRYVLGVRAAQLHHQHOLLPGLLRSLQDLHEEMACILKEILQEYLEISLVQDE 240
Db 181 AHNRYVLGVRAAQLHHQHOLLPGLLRSLQDLHEEMACILKEILQEYLEISLVQDE 240
Qy 241 VVAITHREMAAARIQPEAEYQGFRLQYGSAPDVPVPCVTFDESLEEGLPELQELQNE 300
Db 241 VVAITHREMAAARIQPEAEYQGFRLQYGSAPDVPVPCVTFDESLEEGLPELQELQNE 300
Qy 301 LTVESVQHTLTSVTDELAVATEMVFRRQEMVTOLQELRNEEENTHPRERVQLLGRQVL 360
Db 301 LTVESVQHTLTSVTDELAVATEMVFRRQEMVTOLQELRNEEENTHPRERVQLLGRQVL 360
Qy 361 QEALQGLQVALCSQAKLQAQOELLQTKLEHLGPGEPVPLVLLQDDRHSSTSSSEOREGGR 420
Db 361 QEALQGLQVALCSQAKLQAQOELLQTKLEHLGPGEPVPLVLLQDDRHSSTSSSEOREGGR 420
Qy 421 TPTLEILKSHISGIFRPKFS----- 440
Db 421 TPTLEILKSHISGIFRPKFS----- 440
Qy 441 -----NLYRLEGEPSPISPLLIDHLLSTOQPLTKK 470
Db 481 LVRESQKQEVYLSVLDGLPRHFI IQSLDNLVLEGEFPSPISPLLIDHLLSTOQPLTKK 540
Qy 471 SGVVLHRAVPKDKVNLHEDVLVGEQIGRGNFGEVFSGRADNTLVAVKSCRETLPPDL 530
Db 541 SGVVLHRAVPKDKVNLHEDVLVGEQIGRGNFGEVFSGRADNTLVAVKSCRETLPPDL 600
Qy 531 KAKFLQEARILKQYSHNPVRLIGVCTQKQPIYIVMELVQGGDFLTLRTGRLRVKTL 590
Db 601 KAKFLQEARILKQYSHNPVRLIGVCTQKQPIYIVMELVQGGDFLTLRTGRLRVKTL 660
Qy 591 LQVGDAAAGMEYLESKCCIIHRDLAARNCLVTEKNVLIKISDFGMSREADGVYAAAGSLR 650
Db 661 LQVGDAAAGMEYLESKCCIIHRDLAARNCLVTEKNVLIKISDFGMSREADGVYAAAGSLR 720
Qy 651 QVPVKWTAPEALNYGRYSSESDDVMSFGILLWETSLGASYPNLSNOOTREFVEKGRPL 710
Db 721 QVPVKWTAPEALNYGRYSSESDDVMSFGILLWETSLGASYPNLSNOOTREFVEKGRPL 780
Qy 711 CPELCPDAVFLMEQCWAYEPGQRPSPSTIIYQELQSIKRRHR 752
Db 781 CPELCPDAVFLMEQCWAYEPGQRPSPSTIIYQELQSIKRRHR 822

RESULT 5

US-10-732-923-13687
; Sequence 13687, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10

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; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13687
; LENGTH: 820
; TYPE: PRT
; ORGANISM: Felis catus
US-10-732-923-13687

Query Match      93.3%; Score 3620; DB 17; Length 820;
Best Local Similarity 85.8%; Pred. No. 1.1e-207;
Matches 705; Conservative 21; Mismatches 24; Indels 72; Gaps 2;

QY 1 MGFSSELCSPOGHVGLQMOEAEALRLLEGMRKMAQRVKSDEYAGLLHHMSLQDGGG 60
DB 1 MGFSSELCSPOGHGAVQMOEAEALRLLEGMRKMAQRVKSDEYAGLLHHMSLQDGG-- 58

QY 61 RAISPSPISQSWAETTSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKYTSQW 120
DB 59 RGTGPPSPISQSWAETTSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKYTSQW 118

QY 121 QOLQOELTKTHSDIEKLSQYRALARDSAQAKRYQEAASKDKDRDKAKDKYVRSWLKLF 180
DB 119 QOLQOELTKTHNQDIEKLSQYRALARDSAQAKRYQEAASKDKDRDKAKDKYVRSWLKLF 178

QY 181 AHNRYVGLVRAAQLHHQHHLQLLPGLLRSQDLHEEMACILKEILOEYLEISSLVQDE 240
DB 179 AHNRYVGLVRAAQLHHQHHLQLLPGLLRSQDLHEEMACILKEILOEYLEISSLVQDE 238

QY 241 VVAIHREMAAAARIQPEAEYQGFRLQYGSAPDVPVCTPDESLLBEGEPLEPGELOLNE 300
DB 239 VVAIHLEMAAAVARIQPEAEYQGFRLQYGSTPDVPCVTPDESLLBEGEPLEPGELOLNE 298

QY 301 LTVESVQHTLTSVTDELAVATEMVFRQEMVTOLQOELNEENTHPRERVOLLGKROVL 360
DB 299 LTVESVQHTLTSVTDELAVATQVLSRQEAVALQRELQNEQNTHPRERVOLLAKQVL 358

QY 361 QEALQGLQALCSQAKLQAOQELLQTKLEHLGFGPEPPVLLQLQDRHSSTSSSQEREGGR 420
DB 359 QEALQALQALCSQAKLQAOQRELLQAKLEQLGFGPEPPVLLQLQDRHSSTSSSQEREGGR 418

QY 421 TPTLEILKSHISGIFRPKFS----- 440
DB 419 TPTLEILKSHISGIFRPKFSPLPPPLQLVPEVQKPLHEQLMYHGALPRAEVAELLTHSGDGF 478

QY 441 -----NLYRLEGEGFPSPILLDHLLSTQOPLTKK 470
DB 479 LVRESQKQBYVLSVLWDGQPRHFIIQSADNLVRLLEGDFASIPLLVDHLLRSQOPLTKK 538

QY 471 SGVYLHRAVPKDKWLVNHDVLVGEIQGRGNFGEVFSGRRLRADNTLVAVKSCRETLPDPL 530
DB 539 SGIVLNRAVPKDKWLVNHDVLVGEIQGRGNFGEVFSGRRLRADNTLVAVKSCRETLPDPI 598

QY 531 KAKFLQEARILKOYSHPNIVRLIGVCTQKQPIYVIMELVQGGDFLFLRTEGARLRVKTL 590
DB 599 KAKFLQEARILKOYSHPNIVRLIGVCTQKQPIYVIMELVQGGDFLFLRTEGARLRMKTL 658

QY 591 LQWVGDAAGMEYLESKCCIHRLDLAARNCLVTEKNVLSDFGMSREEDGVVAAAGGLR 650
DB 659 LQWVGDAAGMEYLESKCCIHRLDLAARNCLVTEKNVLSDFGMSREEDGVVAAAGGLR 718

QY 651 QVPVKWTAPEALNRYGYSSESVDVMSFGILLWETFSLGASYPNLSNQQTREFVEKGRPL 710
DB 719 QVPVKWTAPEALNRYGYSSESVDVMSFGILLWETFSLGASYPNLSNQQTREFVEKGRPL 778

RESULT 6
US-10-732-923-13688
; Sequence 13688, Application US/10732923
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; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13688
; LENGTH: 820
; TYPE: PRT
; ORGANISM: Felis catus
US-10-732-923-13688

Query Match      93.3%; Score 3620; DB 17; Length 820;
Best Local Similarity 85.8%; Pred. No. 1.1e-207;
Matches 705; Conservative 21; Mismatches 24; Indels 72; Gaps 2;

QY 1 MGFSSELCSPOGHVGLQMOEAEALRLLEGMRKMAQRVKSDEYAGLLHHMSLQDGGG 60
DB 1 MGFSSELCSPOGHGAVQMOEAEALRLLEGMRKMAQRVKSDEYAGLLHHMSLQDGG-- 58

QY 61 RAISPSPISQSWAETTSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKYTSQW 120
DB 59 RGTGPPSPISQSWAETTSQTEGLSRLLRQHAEDLNSGPLSKLSLLIRERQQLRKYTSQW 118

QY 121 QOLQOELTKTHSDIEKLSQYRALARDSAQAKRYQEAASKDKDRDKAKDKYVRSWLKLF 180
DB 119 QOLQOELTKTHNQDIEKLSQYRALARDSAQAKRYQEAASKDKDRDKAKDKYVRSWLKLF 178

QY 181 AHNRYVGLVRAAQLHHQHHLQLLPGLLRSQDLHEEMACILKEILOEYLEISSLVQDE 240
DB 179 AHNRYVGLVRAAQLHHQHHLQLLPGLLRSQDLHEEMACILKEILOEYLEISSLVQDE 238

QY 241 VVAIHREMAAAARIQPEAEYQGFRLQYGSAPDVPVCTPDESLLBEGEPLEPGELOLNE 300
DB 239 VVAIHLEMAAAVARIQPEAEYQGFRLQYGSTPDVPCVTPDESLLBEGEPLEPGELOLNE 298

QY 301 LTVESVQHTLTSVTDELAVATEMVFRQEMVTOLQOELNEENTHPRERVOLLGKROVL 360
DB 299 LTVESVQHTLTSVTDELAVATQVLSRQEAVALQRELQNEQNTHPRERVOLLAKQVL 358

QY 361 QEALQGLQALCSQAKLQAOQELLQTKLEHLGFGPEPPVLLQLQDRHSSTSSSQEREGGR 420
DB 359 QEALQALQALCSQAKLQAOQRELLQAKLEQLGFGPEPPVLLQLQDRHSSTSSSQEREGGR 418

QY 421 TPTLEILKSHISGIFRPKFS----- 440
DB 419 TPTLEILKSHISGIFRPKFSPLPPPLQLVPEVQKPLHEQLMYHGALPRAEVAELLTHSGDGF 478

QY 441 -----NLYRLEGEGFPSPILLDHLLSTQOPLTKK 470
DB 479 LVRESQKQBYVLSVLWDGQPRHFIIQSADNLVRLLEGDFASIPLLVDHLLRSQOPLTKK 538

QY 471 SGVYLHRAVPKDKWLVNHDVLVGEIQGRGNFGEVFSGRRLRADNTLVAVKSCRETLPDPL 530
DB 539 SGIVLNRAVPKDKWLVNHDVLVGEIQGRGNFGEVFSGRRLRADNTLVAVKSCRETLPDPI 598

QY 531 KAKFLQEARILKOYSHPNIVRLIGVCTQKQPIYVIMELVQGGDFLFLRTEGARLRVKTL 590
DB 599 KAKFLQEARILKOYSHPNIVRLIGVCTQKQPIYVIMELVQGGDFLFLRTEGARLRMKTL 658

QY 591 LQWVGDAAGMEYLESKCCIHRLDLAARNCLVTEKNVLSDFGMSREEDGVVAAAGGLR 650
DB 659 LQWVGDAAGMEYLESKCCIHRLDLAARNCLVTEKNVLSDFGMSREEDGVVAAAGGLR 718

QY 651 QVPVKWTAPEALNRYGYSSESVDVMSFGILLWETFSLGASYPNLSNQQTREFVEKGRPL 710
DB 719 QVPVKWTAPEALNRYGYSSESVDVMSFGILLWETFSLGASYPNLSNQQTREFVEKGRPL 778

711 CPCLCPDAVFLRMEQCWAYEPGQRPFSFTIYQELQSIKXHR 752
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Db 779 CPCLCPDAVFLMBOCWAYEPGQRPFSAYIQELQSIKRRHR 820
 RESULT 7
 US-10-732-923-13665
 ; Sequence 13665, Application US/10732923
 ; Publication No. US20050108791A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edgerton, Michael D
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
 ; FILE REFERENCE: 38-15(52796)C
 ; CURRENT APPLICATION NUMBER: US/10/732,923
 ; CURRENT FILING DATE: 2003-12-10
 ; PRIOR APPLICATION NUMBER: 10/310,154
 ; PRIOR FILING DATE: 2002-12-04
 ; NUMBER OF SEQ ID NOS: 24149
 ; SEQ ID NO 13665
 ; LENGTH: 824
 ; TYPE: PRT
 ; ORGANISM: Gallus gallus
 US-10-732-923-13665
 Query Match 67.9%; Score 2635; DB 17; Length 824;
 Best Local Similarity 62.7%; Pred. No. 6.9e-149;
 Matches 518; Conservative 99; Mismatches 133; Indels 76; Gaps 3;
 QY 1 MGFSELCSPQGHGVLOQMGEAEURLLEGMRKMAQRVKSDREYAGLLHHM----SLQDS 56
 DB 1 MGFGEPLWCXPGHSELURLQDSEURLLELMKKMWSQRAKSDREYAGMLHHMFQLEKQEG 60
 QY 57 GGOSRAISPDPSPISQSWAEITSTQTEGLSRLLRQHAEDLNSGFLSKLLIRERQQLRKY 116
 DB 61 LGHLRATDSHQIGESWVWLASQETETLSQTLRRHAELAAGPLAKLSLIRDKQQLRAKF 120
 QY 117 SEQWQQLQOEBLTKTHSQDI EKLSQYRALARDSAQAKRYQOESKDKDRKAKDKYVRS 176
 DB 121 SEQWQQLSQEYARTTQOEMKLAQYRSVRDSTQAKRYQOESKDKEREKAKYVRS 180
 QY 177 WKLFPAHNRYVGVRAAQLHQQHHLQLLPGLLSLQDHLHEEMACILKEILQYLEISS 236
 DB 181 WKLYALNQVYLA VRAAALHHHHYQALPTLHESLYSLOQEMVVLKELIGEYCSISS 240
 QY 237 VQDEVVAIHREMAAAAARI OPEAEYQOGLFYGSAPDVPVCTFDESLLLEGEPELPEGL 296
 DB 241 VQEDVLAHQEVAHAVEMIDPATEYSFVQCHRYDSEVPVAVT FDESLLLEGEPELPEGL 300
 QY 297 QLNELTVESVOHTLTSVTDELAVATEMVFRQEMVTOLOQELRNEENTHPRVRVQLGK 356
 DB 301 QLNELTTESVQHSLTSTEEELLASREAVSSKEQRWELQVRELGEELALSPGERVHLGK 360
 QY 357 ROVLQOEAQLOVALCSQAKLOAQOELLQTLKHLHGPEPPVLLQDDRHSTSSSQER 416
 DB 361 ROGLQEAQQQLQGLVCAQAKLQAOQDMLANKLAELSGSEPPALPQEDRQSVGSTDOO 420
 QY 417 EGGRTPTLEILKSHISGIFRPKFS----- 440
 DB 421 SG--VTALETIKNHISGIFSPRFSLPVPVPLIPEVQKPLCQAWYHGAI PRSEVQELLKC 478
 QY 441 -----NLYRLEGEGFPSPILPIDHLLSTQOP 466
 DB 479 SGDFLVRRESQKQEVYLSVLWDGQPRHFIIQAADNLYRLEGEGFPPTPLPIDHLLSQOP 538
 QY 467 LTKKSGVYLHRAVPKDKWVLNHHEDLVGEQIGRGNFGEVSGRLRADNTLVAVKSCRETL 526
 DB 539 ITRKSGVLTRAVLKDQWVLNHHEDVLGERIGRGNFGEVSGRLRADNTLVAVKSCRETL 598
 QY 527 PPDLKAKFLQEARILKQYSHENIVRLIGVCTQKQPIYIVMELVGGDFLFLRTEGARLR 586
 DB 599 PPELKAFLQEARILKQYNHNPVRLIGVCTQKQPIYIVMELVGGDFLFLRSEGPHLK 658
 QY 587 VKTLLQWGVDAAGMEYLESKCCITHRDLAARNCLVTEKNVLKISDFGMSREEADGVYAA 646

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QY 527 PDLKAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLFTURTEGARLR 586
Db 673 PPELAKAKFLQEARILKQCNHPNIVRLIGVCTQKQPIYIVMELVQGGDFLFTURTEGARLR 732
QY 587 VTKLLQWGDAAAGMEYLESKCCIHRLDAAARCLVTEKNVLSIDFGMSREADGVYAAAS 646
Db 733 MKKLIKMDNAAAGMEYLESKCHIRDLAARCLVTEKNVLSIDFGMSRQEDGVYAST 792
QY 647 GGLRQVPVKWTAPEALNYGRYSSESVDWMSFGILLMETFSLGASPPYNLSNQOTREFVEKG 706
Db 793 GGMKQIPVKWTAPEALNYGWYSSESVDWMSFGILLWEAFSLGAVPYANLSNQOTREAEIOG 852
QY 707 GRLLPCPELCPDAVFRMLMEQCWAYEPGQRPSPSTIYQELQSIRKRR 752
Db 853 VRLEPPQCPEDVYRLMQRWCWEYDHPHRRPSFGAVHQDLIAIRKRR 898

RESULT 9
US-10-732-923-13482
; Sequence 13482, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13482
; TYPE: PRT
; ORGANISM: Fujinami sarcoma virus
US-10-732-923-13482

Query Match 66.3%; Score 2570; DB 17; Length 873;
Best Local Similarity 61.4%; Pred. No. 5.6e-145;
Matches 507; Conservative 106; Mismatches 137; Indels 76; Gaps 3;

QY 1 MGFSSSELCSPOGHVGLQMQEAEALRLLEGMRKMAQRVKSDEYAGLLHHM----SLQDS 56
Db 50 MGFPELWCPKGHSELRLQDSSELRLLELMKMKWSQRAKSDREYAGMLHHMFSLQEKQEG 109
QY 57 GGQSRAPSPDPSISQSWAEITSQTEGLSLRLRQHAEDLNSGLSKLSLLIRERQQLRKY 116
Db 110 LGHLRATDHSQIGESWVVLASQTETLSQTLRRHAEALAGPLAKLSILIRDKQLRKVF 169
QY 117 SEQWQLOQELTKTHSQDIKLSQYRALARDSAQAKRYQKAKDKDKAKDKYVRS 176
Db 170 SEQWQLOQELTKTHSQDIKLSQYRALARDSAQAKRYQKAKDKDKAKDKYVRS 229
QY 177 WKLFAHNNRYVLGVRAAQHQQHQLLPLGLLSRLQDLHEMACILKEILQELYS 236
Db 230 SKLYALHNQYVLAVQAAALHHHHYQALPTLHESLYSLQGBMVLVLKEILGEYCSITS 289
QY 237 VQDEVVAIHREMAAARAOPEAEYOGFLRQYGSAPDVPVCTTFDESLEECEPLEPCEL 296
Db 290 VQEDVLAHQVAHVMIDPATYESSFVQCHRYDSEVPVPTFDESLEEAESELPCEL 349
QY 297 QLNELTVESVQHTLTSTVDLAVATEMVFRRQEMVTQLOQELRNEENTHPRERVOLLGK 356
Db 350 QLNELTVESVQHTLTSTVDLAVATEMVFRRQEMVTQLOQELRNEENTHPRERVOLLGK 409
QY 417 EGGRTPTLETKHSHIGIFRPKFS----- 440
Db 470 SG--VTALKTIKHNIGSIFRPSLPVPPVPLIPEVQKPLCQQAQVHGAIPRSEVQELLKY 527
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QY 441 -----NLYRLEGEGFPSPILIDHLLSTQOP 466
Db 528 SGDFLVRESQKQBYVLSVLWDGQPRHFIQAADNLYRLEDDGLPTIPLIDHLLSQORP 587
QY 467 LTKKSGVVLHRAVPKDWLNHEDVLGEOIGRGNTEGEVSGRLRADNTLVAVKSCRETL 526
Db 588 ITRKSGVLTRAVLKDWLNHEDVLLGERIGRGNTEGEVSGRLRADNTLVAVKSCRETL 647
QY 527 PDLKAKFLQEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLFTURTEGARLR 586
Db 648 PPELAKAKFLQEARILKQCNHPNIVRLIGVCTQKQPIYIVMELVQGGDFLFTURTEGARLR 707
QY 587 VTKLLQWGDAAAGMEYLESKCCIHRLDAAARCLVTEKNVLSIDFGMSREADGVYAAAS 646
Db 708 MKKLIKMDNAAAGMEYLESKCHIRDLAARCLVTEKNVLSIDFGMSRQEDGVYAST 767
QY 647 GGLRQVPVKWTAPEALNYGRYSSESVDWMSFGILLMETFSLGASPPYNLSNQOTREFVEKG 706
Db 768 GGMKQIPVKWTAPEALNYGWYSSESVDWMSFGILLWEAFSLGAVPYANLSNQOTREAEIOG 827
QY 707 GRLLPCPELCPDAVFRMLMEQCWAYEPGQRPSPSTIYQELQSIRKRR 752
Db 828 VRLEPPQCPEDVYRLMQRWCWEYDHPHRRPSFGAVHQDLIAIRKRR 873

RESULT 10
US-10-732-923-13480
; Sequence 13480, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13480
; TYPE: PRT
; ORGANISM: Fujinami sarcoma virus
US-10-732-923-13480

Query Match 66.0%; Score 2561; DB 17; Length 873;
Best Local Similarity 61.3%; Pred. No. 1.9e-144;
Matches 506; Conservative 106; Mismatches 138; Indels 76; Gaps 3;

QY 1 MGFSSSELCSPOGHVGLQMQEAEALRLLEGMRKMAQRVKSDEYAGLLHHM----SLQDS 56
Db 50 MGFPELWCPKGHSELRLQDSSELRLLELMKMKWSQRAKSDREYAGMLHHMFSLQEKQEG 109
QY 57 GGQSRAPSPDPSISQSWAEITSQTEGLSLRLRQHAEDLNSGLSKLSLLIRERQQLRKY 116
Db 110 LGHLRATDHSQIGESWVVLASQTETLSQTLRRHAEALAGPLAKLSILIRDKQLRKVF 169
QY 117 SEQWQLOQELTKTHSQDIKLSQYRALARDSAQAKRYQKAKDKDKAKDKYVRS 176
Db 170 SEQWQLOQELTKTHSQDIKLSQYRALARDSAQAKRYQKAKDKDKAKDKYVRS 229
QY 177 WKLFAHNNRYVLGVRAAQHQQHQLLPLGLLSRLQDLHEMACILKEILQELYS 236
Db 230 SKLYALHNQYVLAVQAAALHHHHYQALPTLHESLYSLQGBMVLVLKEILGEYCSITS 289
QY 237 VQDEVVAIHREMAAARAOPEAEYOGFLRQYGSAPDVPVCTTFDESLEECEPLEPCEL 296
Db 290 VQEDVLAHQVAHVMIDPATYESSFVQCHRYDSEVPVPTFDESLEEAESELPCEL 349
QY 297 QLNELTVESVQHTLTSTVDLAVATEMVFRRQEMVTQLOQELRNEENTHPRERVOLLGK 356
Db 350 QLNELTVESVQHTLTSTVDLAVATEMVFRRQEMVTQLOQELRNEENTHPRERVOLLGK 409
QY 357 RQVLQELQGLQVALCSQAKLQAOQELLOTKLEHLGPGEPVPLVLLQDDRHSSTSSQER 416
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Db 410 RQUREAQOQGLVCAQAKLQORDMLANKLAELGSEPPALPQEDRQASARSTDOER 469
Qy 417 EGGRTPTLEIKSHISGIFRPKFS-
Db 470 SG--VTALKTIKNIHISGIFSPRFSLPVPLIPEVQKPLCQQAHYHGAIPRSEVOELLKY 527
Qy 441 -----NLYRLEGEPPSPILLIDHLLSTQOP 466
Db 528 SGDFLVRESQKQYVLSVLWDGQPRHFIIQAADNLYRLLEDGLPTIPLLIHLLQSORP 587
Qy 467 LTKKSGVVLHRAVPKQKWLNHEDVLGEOIGRGNFGEVPSGRLRADNTLVAVKSCRETL 526
Db 588 ITRKSGVILTRAVLKDQKWLNHEDVLGGERIGRGNFGEVPSGRLRADNTLVAVKSCRETL 647
Qy 527 PDLKAKFLOEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLFLRTGEGARLR 586
Db 648 PDLKAKFLOEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLFLRTGEGARLR 707
Qy 587 VTKLLQVGDAAAAGMEYLESKCCIHRDLAARNCLVTEKNVTKISDFGMSREEDGVYAAAS 646
Db 708 MKKLIKMMENAAAAGMEYLESKCHCIHRDLAARNCLVTEKNVTKISDFGMSREEDGVYAAAS 767
Qy 647 GGLRQVPVKWTAPEALNYGRYSSESVDWVSFGILLWETFSLGASYPNLSNQOTREFVEKG 706
Db 768 GGMKQIPVKWTAPEALNYGRYSSESVDWVSFGILLWETFSLGASYPNLSNQOTREFVEKG 827
Qy 707 GRLEPCPELCPDAVFRLEMCQWAVEPQORPSFTIYQELQSIKRRHR 752
Db 828 VRLEPPQCPEDVYRLMQRCEYDPRRPSFGAVHQDLIAIRKRRH 873

RESULT 11
US-10-732-923-13479
; Sequence 13479, Application US/10732923
; Publication No. US2005010879A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13479
; LENGTH: 1182
; TYPE: PRT
; ORGANISM: Fufinami sarcoma virus
US-10-732-923-13479

Query Match 66.0%; Score 2561; DB 17; Length 1182;
Best Local Similarity 61.3%; Pred. No. 2,7e-144;
Matches 506; Conservative 106; Mismatches 138; Indels 76; Gaps 3;

Qy 1 MGFSSSELCSPOGHVGLVQMQEAEIRLLEGKMKMAQRVKSDEYAGLLHMSLQDSGQS 56
Db 359 MGFPELWCPKGHTELLRLQDSLELRLLLEMKWMSQRAKSDREYAGLLHMSLQDSGQS 418
Qy 57 GQSRALSPDISQSWAETSQTEGLRLLRQHAEDLNSGPLSKLLIRERQOLKTY 116
Db 419 LGHLRATDHSQIGESWVWLASQTEGLRLLRQHAEDLNSGPLSKLLIRERQOLKTY 478
Qy 117 SEWQOQLQELTKTHSODIEKLKSOYRALARDSQAQAKRYQEAASKDKDRKADKYVRS 176
Db 479 SEWQOQLQELTKTHSODIEKLKSOYRALARDSQAQAKRYQEAASKDKDRKADKYVRS 538
Qy 177 WKLFANHRNYVLGVRQAQLHHQHLLQLLGLRLSLQDLHEEMACILKEIQLEYLSS 236
Db 539 SKLVALHNQYVLAQAAALHHHHYQRALPTLHESLYSLQEQWVVLKEILGEYCSITSL 598
Qy 237 VQDEVAIHREMAAAAARIQEABYQGLFQRYGAPDVPVPCVTPDESILLEGEPLEPGE 296

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Db 599 VQEDVLAIHOKVAHVMEMIDPATEYSSFVOCHRYDSEVPVPAVTFDBSLLBEAENLEPGE 658
Qy 297 QNLNLTVESVQHTLTSVTDLAVATEMVFRRQEMVTQLQOELRNEENTHPRERVQLLGK 356
Db 659 QNLNLTIESVQHTLTSVTDLAVATEMVFRRQEMVTQLQOELRNEENTHPRERVQLLGK 718
Qy 357 RQVLOALQGLQVALCSQAKLQAOQELLQTKLHGLGEGEPPVLLQLDDRHSSSSSQER 416
Db 719 RQVLOALQGLQVALCSQAKLQAOQELLQTKLHGLGEGEPPVLLQLDDRHSSSSSQER 778
Qy 417 EGGRTPTLEIKSHISGIFRPKFS-
Db 779 SG--VTALKTIKNIHISGIFSPRFSLPVPLIPEVQKPLCQQAHYHGAIPRSEVOELLKY 836
Qy 441 -----NLYRLEGEPPSPILLIDHLLSTQOP 466
Db 837 SGDFLVRESQKQYVLSVLWDGQPRHFIIQAADNLYRLLEDGLPTIPLLIHLLQSORP 896
Qy 467 LTKKSGVVLHRAVPKQKWLNHEDVLGEOIGRGNFGEVPSGRLRADNTLVAVKSCRETL 526
Db 897 ITRKSGVILTRAVLKDQKWLNHEDVLGGERIGRGNFGEVPSGRLRADNTLVAVKSCRETL 956
Qy 527 PDLKAKFLOEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLFLRTGEGARLR 586
Db 957 PDLKAKFLOEARILKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLFLRTGEGARLR 1016
Qy 587 VTKLLQVGDAAAAGMEYLESKCCIHRDLAARNCLVTEKNVTKISDFGMSREEDGVYAAAS 646
Db 1017 MKKLIKMMENAAAAGMEYLESKCHCIHRDLAARNCLVTEKNVTKISDFGMSREEDGVYAAAS 1076
Qy 647 GGLRQVPVKWTAPEALNYGRYSSESVDWVSFGILLWETFSLGASYPNLSNQOTREFVEKG 706
Db 1077 GGMKQIPVKWTAPEALNYGRYSSESVDWVSFGILLWETFSLGASYPNLSNQOTREFVEKG 1136
Qy 707 GRLEPCPELCPDAVFRLEMCQWAVEPQORPSFTIYQELQSIKRRHR 752
Db 1137 VRLEPPQCPEDVYRLMQRCEYDPRRPSFGAVHQDLIAIRKRRH 1182

RESULT 12
US-10-732-923-13452
; Sequence 13452, Application US/10732923
; Publication No. US2005010879A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13452
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Gardner-Arnstein feline sarcoma virus
US-10-732-923-13452

Query Match 63.9%; Score 2479; DB 17; Length 609;
Best Local Similarity 61.7%; Pred. No. 1e-139;
Matches 507; Conservative 11; Mismatches 14; Indels 290; Gaps 3;

Qy 1 MGFSSSELCSPOGHVGLVQMQEAEIRLLEGKMKMAQRVKSDEYAGLLHMSLQDSGQS 60
Db 8 MGFSSSELCSPOGHVGLVQMQEAEIRLLEGKMKMAQRVKSDEYAGLLHMSLQDSGQS 65
Qy 61 RAISPSPISQSWAETSQTEGLRLLRQHAEDLNSGPLSKLLIRERQOLKTYSEW 120
Db 66 RGTGYPSPISQSWAETSQTEGLRLLRQHAEDLNSGPLSKLLIRERQOLKTYSEW 125
Qy 121 QLOQELTKTHSODIEKLKSOYRALARDSQAQAKRYQEAASKDKDRKADKYVRSWLK 180
Db 126 QLOQELTKTHSODIEKLKSOYRALARDSQAQAKRYQEAASKDKDRKADKYVRSWLK 173

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181 AHNRYVLGVRAAQLHHQHLLPGLLRSLQDLHEEMACILKEILQYLEISSLVQDE 240
 174 ----- 173
 241 VVAIHREMAAAARIQPEAEYQGFLOYGSAPDVPVPCVTFDESLLBEGEPLEFGLQNE 300
 174 ----- 173
 301 LTVESVQHTLTSVTDLAVATEMVFRRQEMVTQLQELRNEEENTHPRERVQLLGRQVL 360
 174 ----- 173
 361 QBALQGLVALCSQAKLQAQOELLQTKLEHLGPGEPPLVLLQDDRHSSTSSQEREGGR 420
 174 ----- 173
 421 TPTLEILKSHISGIFRPKFS----- 440
 208 TPTLEILKSHISGIFRPKFSPLPPLQVLPEVQKPLHEQLWYHGALPRAEVAELLTHSGDF 267
 441 -----
 268 LVRESQKQEVYLVWMDQGRPHFI IQSADNLVYRPEGDFASIPLLVDHLRSQOPLTKK 327
 471 SGVVLHRAVPKDKWLNHEDVLVGEQIGRGNGFVFSGLRADNTLVAVKSCRETLPPDL 530
 328 SGVVLNRAVPKDKWLNHEDVLVGEQIGRGNGFVFSGLRADNTLVAVKSCRETLPPDI 387
 531 KAKFLOEAKILKQYSHPNIVRLIGVCTQKQPIYIYVWELVQGGDFLTLRTGAGLRVKT 590
 388 KAKFLOEAKILKQYSHPNIVRLIGVCTQKQPIYIYVWELVQGGDFLTLRTGAGLRVKT 447
 591 LQWVGDAAGMEYLESKCCIHRLDAAARNCLVTEKNVLTISDFGMSREADGYAASGGLR 650
 448 LQWVGDAAGMEYLESKCCIHRLDAAARNCLVTEKNVLTISDFGMSREADGYAASGGLR 507
 651 QVPVKWTAPEALNYGRYSSESVDWVSGILLWTFSLGASFPYVNLNQOTREFVEKGRRLP 710
 508 QVPVKWTAPEALNYGRYSSESVDWVSGILLWTFSLGASFPYVNLNQOTREFVEKGRRLP 567
 711 CPCLCPDAVFLMEQWAVEPGORPSFTIYQELQSIKRRHR 752
 568 CPCLCPDAVFLMEQWAVEPGORPSFTIYQELQSIKRRHR 609
 RESULT 13
 US-10-732-923-13461
 ; Sequence 13461, Application US/10732923
 ; Publication No. US20050108791A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edgerton, Michael D
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
 ; FILE REFERENCE: 38-15(52796)C
 ; CURRENT APPLICATION NUMBER: US/10/732,923
 ; CURRENT FILING DATE: 2003-12-10
 ; PRIOR APPLICATION NUMBER: 10/310,154
 ; PRIOR FILING DATE: 2002-12-04
 ; NUMBER OF SEQ ID NOS: 24149
 ; SEQ ID NO 13461
 ; LENGTH: 957
 ; TYPE: PRP
 ; ORGANISM: Gardner-Arnstein feline leukemia oncovirus B
 US-10-732-923-13461
 Query Match 63.9%; Score 2479; DB 17; Length 957;
 Best local Similarity 61.7%; Pred. No. 1.7e-139;
 Matches 507; Conservative 11; Mismatches 14; Indels 290; Gaps 3;
 1 MGFSSSELCSQGHVILQQWQAEALRLLEGRKWAQVKSDEYAGLLHMSLODSSGQS 60
 356 MGFSSSELCSQGHVILQQWQAEALRLLEGRKWAQVKSDEYAGLLHMSLODSSGQS-- 413

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OM nucleic - nucleic search, using sw model

Run on: August 9, 2005, 20:15:00 ; Search time 2010.27 Seconds
(without alignments)
7274.725 Million cell updates/sec

Title: US-10-660-763-1_COPY_72_2327

Perfect score: 2256

Sequence: 1 atgggtctctcttgagct.....gcacgaaagcgatcg 2256

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US10J_PUBCOMB.seq:*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2256	100.0	2674	13	US-10-003-295-1
2	2256	100.0	2674	18	US-10-660-763-1
3	2023.4	89.7	2889	16	US-10-240-965-256
4	328.8	14.6	2950	21	US-10-887-553A-240
5	326.8	14.5	449	10	US-09-918-995-1503
6	296.2	13.1	361	9	US-09-948-802-5
7	296.2	13.1	361	15	US-10-121-925-5

8	271.6	12.0	1779	18	US-10-280-576-19	Sequence 19, Appl
9	227.2	10.1	15297	13	US-10-003-295-3	Sequence 3, Appl
10	227.2	10.1	15297	18	US-10-660-763-3	Sequence 3, Appl
11	201.2	8.9	3875	15	US-10-101-510-525	Sequence 525, App
12	198	8.8	2955	19	US-10-384-339C-1	Sequence 1, Appl
13	198	8.8	3370	9	US-09-967-768A-144	Sequence 144, App
14	198	8.8	3370	16	US-10-354-358-101	Sequence 101, App
15	198	8.8	3370	16	US-10-210-120-19	Sequence 19, Appl
16	198	8.8	3370	19	US-10-776-827-82	Sequence 82, Appl
17	198	8.8	3370	20	US-10-473-974-219	Sequence 219, App
18	198	8.8	3370	21	US-10-843-641A-6289	Sequence 6289, Ap
19	198	8.8	3370	22	US-10-909-035-19	Sequence 2, Appl
20	185.4	8.2	3042	19	US-10-384-339C-2	Sequence 29, Appl
21	185.4	8.2	3921	10	US-09-921-406C-29	Sequence 222, App
22	185.4	8.2	3921	15	US-10-007-926A-222	Sequence 19, Appl
23	185.4	8.2	3921	16	US-10-269-909-19	Sequence 1, Appl
24	185.4	8.2	3921	17	US-10-366-288-1	Sequence 1036, Ap
25	185.4	8.2	3921	17	US-10-172-118-1036	Sequence 1036, Ap
26	185.4	8.2	3921	18	US-10-342-887-1036	Sequence 19, App
27	185.4	8.2	3921	18	US-10-287-226-319	Sequence 1, Appl
28	185.4	8.2	3921	19	US-10-648-593-1	Sequence 223, App
29	185.4	8.2	3921	20	US-10-473-974-223	Sequence 5, Appl
30	185.4	8.2	3921	21	US-10-616-403-5	Sequence 1, Appl
31	185.4	8.2	3935	21	US-10-897-711-1	Sequence 24, Appl
32	176.2	7.6	1518	18	US-10-280-576-24	Sequence 3, Appl
33	174.6	7.7	816	19	US-10-377-268-3	Sequence 4, Appl
34	174.6	7.7	1050	19	US-10-377-268-4	Sequence 8, Appl
35	174.6	7.7	3030	16	US-10-325-430-8	Sequence 1, Appl
36	174.6	7.7	3416	8	US-08-987-689A-1	Sequence 1, Appl
37	174.6	7.7	3416	15	US-10-292-524-1	Sequence 2, Appl
38	174.6	7.7	3416	17	US-10-464-805-2	Sequence 1483, Ap
39	174.6	7.7	3416	17	US-10-305-720-1483	Sequence 1, Appl
40	174.6	7.7	3416	21	US-10-860-066-1	Sequence 51, Appl
41	174.6	7.7	3544	14	US-10-161-803-51	Sequence 13, Appl
42	174.6	7.7	4089	17	US-10-291-808-13	Sequence 7, Appl
43	174.6	7.7	4089	19	US-10-620-052A-7	Sequence 52, Appl
44	174.6	7.7	4151	14	US-10-161-803-52	Sequence 7, Appl
45	174.6	7.7	4151	16	US-10-325-430-7	

ALIGNMENTS

RESULT 1

US-10-003-295-1
; Sequence 1, Application US/10003295
; Publication No. US20020168741A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIV
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-003-295-1

Query Match	100.0%	Score 2256;	DB 13;	Length 2674;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 2256;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGGGCTTCTTCTTCTGAGCTGTGACGCGCCAGCGGCTCTCTGACGAAATGCAG	60	
Db	72	ATGGGCTTCTTCTTCTGAGCTGTGACGCGCCAGCGGCTCTCTGACGAAATGCAG	131	
Qy	61	GAGCGCGAGCTTCTGCTTACTTCTGAGGCGATGAGAAATGATGCCCGCGGCTCAAGAT	120	

132 GAGGCGAGCTTCGTCTACTGAGGGGATGAGAAAGTGGATGGCCAGCGGTCAGAGT 191
 121 GACAGGAGTATGACAGGATCTGCTTACCAATATGCTCCGACAGGACAGTGGGGCCAGAGC 180
 192 GACAGGAGTATGACAGGATCTGCTTACCAATATGCTCCGACAGGACAGTGGGGCCAGAGC 251
 181 CGGGCCATCAGCCCTGACAGCCCATCAGTCTGCTGAGTCTGCTGAGATCAGCAGCCAACT 240
 252 CGGGCCATCAGCCCTGACAGCCCATCAGTCTGCTGAGTCTGCTGAGATCAGCAGCCAACT 311
 241 GAGGCTGAGCCCTGCTGCTGAGGAGCAGCAGCAGGATCTGAACTCAGGCGCCCTGAGC 300
 312 GAGGCTGAGCCCTGCTGCTGAGGAGCAGCAGCAGGATCTGAACTCAGGCGCCCTGAGC 371
 301 AAGCTGAGCCTGCTGCTGAGGAGCAGCAGCAGGATCTGAACTCAGGCGCCCTGAGC 360
 372 AAGCTGAGCCTGCTGCTGAGGAGCAGCAGCAGGATCTGAACTCAGGCGCCCTGAGC 431
 361 CAGCAGCTGACAGGAGCTCAGCAGGAGCAGCAGGATCTGAACTCAGGCGCCCTGAGC 420
 432 CAGCAGCTGACAGGAGCTCAGCAGGAGCAGCAGGATCTGAACTCAGGCGCCCTGAGC 491
 421 CAGTACCGAGCTCTGCAAGGAGCAGTCCAGGAGCAGTCCAGGAGCAGCAGCAGCAGC 480
 492 CAGTACCGAGCTCTGCAAGGAGCAGTCCAGGAGCAGTCCAGGAGCAGCAGCAGCAGC 551
 481 AAGAGCAAGGAGCAGTCCAGGAGCAGTCCAGGAGCAGTCCAGGAGCAGCAGCAGCAGC 540
 552 AAGAGCAAGGAGCAGTCCAGGAGCAGTCCAGGAGCAGTCCAGGAGCAGCAGCAGCAGC 611
 541 GCTACCAACACCGCTATGCTGCGGAGCAGTCCAGGAGCAGTCCAGGAGCAGCAGCAGC 600
 612 GCTACCAACACCGCTATGCTGCGGAGCAGTCCAGGAGCAGTCCAGGAGCAGCAGCAGC 671
 601 CACAGCTCTGCTGCTGCGGAGCAGTCCAGGAGCAGTCCAGGAGCAGTCCAGGAGCAGC 660
 672 CACAGCTCTGCTGCTGCGGAGCAGTCCAGGAGCAGTCCAGGAGCAGTCCAGGAGCAGC 731
 661 TGATCTCTGAGGAGATCTGAGGAGATCTGAGGAGATCTGAGGAGATCTGAGGAGATGAG 720
 732 TGATCTCTGAGGAGATCTGAGGAGATCTGAGGAGATCTGAGGAGATCTGAGGAGATGAG 791
 721 GTGGTGGCATTCACCGGAGATGCTGAGGAGATCTGAGGAGATCTGAGGAGATGAG 780
 792 GTGGTGGCATTCACCGGAGATGCTGAGGAGATCTGAGGAGATCTGAGGAGATGAG 851
 781 TACCAAGGCTTCTGCGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAG 840
 852 TACCAAGGCTTCTGCGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAG 911
 841 GATGAGTCTGCTGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAG 900
 912 GATGAGTCTGCTGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAG 971
 901 CTGATCTGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAG 960
 972 CTGATCTGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAG 1031
 961 ACCGAGATGCTGCTGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAG 1020
 1032 ACCGAGATGCTGCTGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAG 1091
 1021 GAGGAGATGCTGCTGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAG 1080
 1092 GAGGAGATGCTGCTGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAG 1151
 1081 CAAGAAGCAGCTGCTGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAG 1140
 1152 CAAGAAGCAGCTGCTGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAG 1211
 1141 CAGGAGATGCTGCTGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAG 1200
 1212 CAGGAGATGCTGCTGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGATGAG 1271

1201 CTCTCTGAGGATGACCGCCATCTCAGCTGCTCTCGGAGCAGGAGCGAGAGGGGGAAGG 1260
 1272 CTCTCTGAGGATGACCGCCATCTCAGCTGCTCTCGGAGCAGGAGCGAGAGGGGGAAGG 1331
 1261 ACACCCACCTGAGATCTTAAAGAGCCACATCTCAGGAATCTTCCGCCCCCAAGTTCTCG 1320
 1332 ACACCCACCTGAGATCTTAAAGAGCCACATCTCAGGAATCTTCCGCCCCCAAGTTCTCG 1391
 1321 AACCTTACCGATCTGGAAGGGGAAAGCTTCTAGCATCTTCTGCTCATCGACCACTA 1380
 1392 AACCTTACCGATCTGGAAGGGGAAAGCTTCTAGCATCTTCTGCTCATCGACCACTA 1451
 1381 CTGAGACCCACGAGCCCTCTCAGGAGAGTGGTGTCTCTGCTGCAAGGGCTGTGCC 1440
 1452 CTGAGACCCACGAGCCCTCTCAGGAGAGTGGTGTCTCTGCTGCAAGGGCTGTGCC 1511
 1441 AAGGACAAAGTGGTGTCTGAAACCATAGAGACCTGTGGTGTGAGCAGATTCGAGGGG 1500
 1512 AAGGACAAAGTGGTGTCTGAAACCATAGAGACCTGTGGTGTGAGCAGATTCGAGGGG 1571
 1501 AACTTTGGCGAAGTGTTCAGCGGACGCTTCCGAGCCGACCAACACCTGTGGCGGTGAAG 1560
 1572 AACTTTGGCGAAGTGTTCAGCGGACGCTTCCGAGCCGACCAACACCTGTGGCGGTGAAG 1631
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 1632 TCTTTGTCGAGAGACGCTTCCACCTGACCTCAAGGCGCAAGTTTCTACAGGAGCGAGATC 1691
 1621 CTGAGGAGATGACGAGCCCTCTGAGGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
 1692 CTGAGGAGATGACGAGCCCTCTGAGGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1751
 1681 CCCATCTACATCTGCTGAGGAGTGTCTGAGGAGGCGACTTCTGAGCTTCTCTCCGACG 1740
 1752 CCCATCTACATCTGCTGAGGAGTGTCTGAGGAGGCGACTTCTGAGCTTCTCTCCGACG 1811
 1741 GAGGGGCGCGCTGCGGAGTGAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
 1812 GAGGGGCGCGCTGCGGAGTGAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1871
 1801 ATGGAGTACCTGAGGAGCAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
 1872 ATGGAGTACCTGAGGAGCAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1931
 1861 GTGACAGAGAAATGTCTGAGATCAGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
 1932 GTGACAGAGAAATGTCTGAGATCAGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1991
 1921 GGGTCTATGACGCTCTGAGGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
 1992 GGGTCTATGACGCTCTGAGGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2051
 1981 GCGCTTAACTAAGGCGCTTCTCTGAGGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
 2052 GCGCTTAACTAAGGCGCTTCTCTGAGGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 2111
 2041 TGAGGAGCTTCTGAGGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
 2112 TGAGGAGCTTCTGAGGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2171
 2101 GAGTTTGTGAGAGGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
 2172 GAGTTTGTGAGAGGGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2231
 2161 AGGCTCTATGAGGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
 2232 AGGCTCTATGAGGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2291
 2221 TACGAGGAGTGTGAGAGATTCGAGAGCGGATCGG 2256
 2292 TACGAGGAGTGTGAGAGATTCGAGAGCGGATCGG 2327

RESULT 2

US-10-660-763-1
; Sequence 1, Application US/10660763
; Publication No. US20040063130A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIV11
; CURRENT APPLICATION NUMBER: US/10/660,763
; CURRENT FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-660-763-1

Query Match 100.0%; Score 2256; DB 18; Length 2674;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGGCTTCTCTTCTGAGCTGTGAGCCGCCAGGGCCACCGGGTCTCTGACGCAAAATGCAG 60
DB 72 ATGGGCTTCTCTTCTGAGCTGTGAGCCGCCAGGGCCACCGGGTCTCTGACGCAAAATGCAG 131
QY 61 GAGGCCGAGCTTCTCTTCTGAGGCGATGAGAAAGTGGATGGCCAGCGGGTCTGAGAT 120
DB 132 GAGGCCGAGCTTCTCTTCTGAGGCGATGAGAAAGTGGATGGCCAGCGGGTCTGAGAT 191
QY 121 GACAGGAGTATGAGGAGCTGCTTACCAATGCTCCCTGAGGACAGTGGGGCCAGAGC 180
DB 192 GACAGGAGTATGAGGAGCTGCTTACCAATGCTCCCTGAGGACAGTGGGGCCAGAGC 251
QY 181 CGGGCCATGAGCTTCTGAGCCGATCAGTCAAGTCTGAGTCTGAGTACACAGCCAAAT 240
DB 252 CGGGCCATGAGCTTCTGAGCCGATCAGTCAAGTCTGAGTCTGAGTACACAGCCAAAT 311
QY 241 GAGGCCGAGCTTCTGAGCCGATCAGTCAAGTCTGAGTCTGAGTACACAGCCAAAT 300
DB 312 GAGGCCGAGCTTCTGAGCCGATCAGTCAAGTCTGAGTCTGAGTACACAGCCAAAT 371
QY 301 AAGCTGAGCTTCTGAGCTTCTGAGCCGATCAGTCAAGTCTGAGTACACAGCCAAAT 360
DB 372 AAGCTGAGCTTCTGAGCTTCTGAGCCGATCAGTCAAGTCTGAGTACACAGCCAAAT 431
QY 361 CAGCAGCTGAGGAGGAGCTCACCAGACCCAGCAGGACATTTGAGAGCTGAGAGC 420
DB 432 CAGCAGCTGAGGAGGAGCTCACCAGACCCAGCAGGACATTTGAGAGCTGAGAGC 491
QY 421 CAGTACCGAGCTTCTGAGCCGATCAGTCAAGTCTGAGTACACAGCCAAAT 480
DB 492 CAGTACCGAGCTTCTGAGCCGATCAGTCAAGTCTGAGTACACAGCCAAAT 551
QY 481 AAGACAAAGGAGCTGAGCAAGGCGCAGGACATTTGAGAGCTGAGAGCCTTTT 540
DB 552 AAGACAAAGGAGCTGAGCAAGGCGCAGGACATTTGAGAGCTGAGAGCCTTTT 611
QY 541 GCTCACCACAAACCGCTATGCTGGGCGTGGGGCTGCGGAGCTTACCAACAGCAGC 600
DB 612 GCTCACCACAAACCGCTATGCTGGGCGTGGGGCTGCGGAGCTTACCAACAGCAGC 671
QY 601 CACGAGCTTCTGCTGGGCGTGGGGCTGCGGAGCTTACCAACAGCAGCAGGATGGCT 660
DB 672 CACGAGCTTCTGCTGGGCGTGGGGCTGCGGAGCTTACCAACAGCAGCAGGATGGCT 731
QY 661 TGCATCTGAGGAGAGTCTTGCAGGAATACCTGAGAGATTAGCAGCTGGTGCAGATGAG 720
DB 732 TGCATCTGAGGAGAGTCTTGCAGGAATACCTGAGAGATTAGCAGCTGGTGCAGATGAG 791

QY 721 GTGGTGGCCATTTCACCGGAGAGTGGCTGAGCTGTGCTGCCGATCCAGCCTGAGGCTGAG 780
DB 792 GTGGTGGCCATTTCACCGGAGAGTGGCTGAGCTGTGCTGCCGATCCAGCCTGAGGCTGAG 851
QY 781 TACCAAGGCTTCTGCGACAGATGAGTGGTCCGACCTGACGCTGCCACCTGCTGTCACGTTTC 840
DB 852 TACCAAGGCTTCTGCGACAGATGAGTGGTCCGACCTGACGCTGCCACCTGCTGTCACGTTTC 911
QY 841 GATGAGTCACTGCTTGAAGGAGGTGAACCGCTGAGAGCTTGGGAGCTTCCAGCTGAACGAG 900
DB 912 GATGAGTCACTGCTTGAAGGAGGTGAACCGCTGAGAGCTTGGGAGCTTCCAGCTGAACGAG 971
QY 901 CTGACTGTGGAGAGCGTGCAGCAGACGCTGACCTCAGTGCAGATGAGCTGGCTGTGGCC 960
DB 972 CTGACTGTGGAGAGCGTGCAGCAGACGCTGACCTCAGTGCAGATGAGCTGGCTGTGGCC 1031
QY 961 ACCGAGATGCTGTTACGGCGGAGGAGATGTTTACCGAGCTGCAACAGGAGCTCCGGAAT 1020
DB 1032 ACCGAGATGCTGTTACGGCGGAGGAGATGTTTACCGAGCTGCAACAGGAGCTCCGGAAT 1091
QY 1021 GAAGAGGAGAAACCCACCCCGGAGCGGGTGCAGCTGCTGGGCAAGAGGCAAGTCTGT 1080
DB 1092 GAAGAGGAGAAACCCACCCCGGAGCGGGTGCAGCTGCTGGGCAAGAGGCAAGTCTGT 1151
QY 1081 CAAGAAAGCTGAGGAGGCTGAGGTTAGCGCTGTGCAGCCAGGCAAGCTGAGGCGCAG 1140
DB 1152 CAAGAAAGCTGAGGAGGCTGAGGTTAGCGCTGTGCAGCCAGGCAAGCTGAGGCGCAG 1211
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DB 1212 CAGGAGTGTGTCAGACCAAGCTGAGGAGCACTGCGGCGCCGCGAGCCCGCTGTGCTG 1271
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QY 1501 AACCTTTGGCGAAGTGTTCAGGGGAGCCCTGCGAGCGGCAACACCTTGTGGGCGTGAAG 1560
DB 1572 AACCTTTGGCGAAGTGTTCAGGGGAGCCCTGCGAGCGGCAACACCTTGTGGGCGTGAAG 1631
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DB 1692 CTGAAGCAGTACAGCACCACCCCAACATCTGCTGCTCATTTGGTGTCTGACCCAGAGCAG 1751
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DB 1752 CCATCTACATCTGATGAGCTTGTGAGGGGGGAGCTTCTGAGCTTCTCCCGCAGC 1811
QY 1741 GAGGGGCGCCGCTGCGGGTGAAGACTCTGCTGAGATGGTGGGGATGACAGTGTCTGGC 1800
DB 1812 GAGGGGCGCCGCTGCGGGTGAAGACTCTGCTGAGATGGTGGGGATGACAGTGTCTGGC 1871
QY 1801 ATGGAGTACCTGAGAGCAAGTGTCTGCATCCACCGGGAACCTGTGCTGTGCGAACTGCTG 1860


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QY 1200 GCTCCTCAGGATGACCGCCACTCCACGTCGTCTCGGAGCAGGAGCGAGGGGGGAAG 1259
Db 1388 GCTCCTCAGGATGACCGCCACTCCACGTCGTCTCGGAGCAGGAGCGAGGGGGGAAG 1447
QY 1260 GACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCGCGCCCAAGTTCTC 1319
Db 1448 GACACCCACGCTGGAGATCCTTAAGAGCCACATCTCAGGAATCTTCGCGCCCAAGTTCTC 1507
QY 1320 G----- 1320
Db 1508 GCTCCCTCCACCGCTGCAGCTCAATTCGGAGGTGCAGAGCCCTGCAATGAGCAGCTGTG 1567
QY 1321 ----- 1320
Db 1568 GTACACGGGGCCATCCCGAGGCGAGAGGTGGTGTGACTGCTGTGTGCACTCTGGGACTT 1627
QY 1321 ----- 1320
Db 1628 CCTGGTCCGGAGAGCCAGGGCAAGCAGGAGTAGCTGCTGTGGTGTGTGGATGTGTCT 1687
QY 1321 -----AACCTGTACCGACTTGAAGGGGAAGGCTT 1349
Db 1688 GCGCCGCACTTCATCATCCAGTCTTTGGATAACCTGTACCGACTGGAAGGGGAAGGCTT 1747
QY 1350 TCCTAGCATTCCTTTGCTCATCGACCACTACTGAGCACCAGCCAGCCCTTCCACCAAGAA 1409
Db 1748 TCCTAGCATTCCTTTGCTCATCGACCACTACTGAGCACCAGCCAGCCCTTCCACCAAGAA 1807
QY 1410 GAGTGGTGTGTCTGTCACAGGCTGTGCCAAGGACAAGTGGTGTCTGAACCATGAGGA 1469
Db 1808 GAGTGGTGTGTCTGTCACAGGCTGTGCCAAGGACAAGTGGTGTCTGAACCATGAGGA 1867
QY 1470 CCTGGTGTGGGTGAGCAGATTTGACGGGGGAACCTTTGGCGAAGTGTTCAGCGGACGCT 1529
Db 1868 CCTGGTGTGGGTGAGCAGATTTGACGGGGGAACCTTTGGCGAAGTGTTCAGCGGACGCT 1927
QY 1530 GCGAGCGGACAAACCTGTGGTGGGTGAAGTCTTGTGAGAGAGCGCTCCCACTGACCT 1589
Db 1928 GCGAGCGGACAAACCTGTGGTGGGTGAAGTCTTGTGAGAGAGCGCTCCCACTGACCT 1987
QY 1590 CAAGGCCAAGTTCTACAGGAAGCGAGGATCCTGAAGCAGTACAGCCACCCCAACATCGT 1649
Db 1988 CAAGGCCAAGTTCTACAGGAAGCGAGGATCCTGAAGCAGTACAGCCACCCCAACATCGT 2047
QY 1650 GCGTCTCATTTGGTGTCTGACCCAGAGAGCCCATCTACATCGTCAATGGAGCTTGTGCA 1709
Db 2048 GCGTCTCATTTGGTGTCTGACCCAGAGAGCCCATCTACATCGTCAATGGAGCTTGTGCA 2107
QY 1710 GGGGGGCGACTTCTGACCTTCTCCGACGAGGAGGGGGCGCGCTGCGGGTGAAGACTCT 1769
Db 2108 GGGGGGCGACTTCTGACCTTCTCCGACGAGGAGGGGGCGCGCTGCGGGTGAAGACTCT 2167
QY 1770 GCTGCAGATGGTGGGATGAGCTGTGCGATGAGTACTTGAGAGCAAGTCTGCTGCAT 1829
Db 2168 GCTGCAGATGGTGGGATGAGCTGTGCGATGAGTACTTGAGAGCAAGTCTGCTGCAT 2227
QY 1830 CCACCGGAGCTGCTGCTCGAACTGCTGCTGTCACAGAGAAAGTCTCTGAAGATCAG 1889
Db 2228 CCACCGGAGCTGCTGCTCGAACTGCTGCTGTCACAGAGAAAGTCTCTGAAGATCAG 2287
QY 1890 TGACTTTGGGATGTCGCGAGAGGAAGCGATGGGGTCTATGACGCTTCAGGGGCGCTCAG 1949
Db 2288 TGACTTTGGGATGTCGCGAGAGGAAGCGATGGGGTCTATGACGCTTCAGGGGCGCTCAG 2347
QY 1950 ACAGTCCCCTGAGTGGACCGCACCTGAGGCGCTTAACTACGCGCGTACTCTCCGA 2009
Db 2348 ACAGTCCCCTGAGTGGACCGCACCTGAGGCGCTTAACTACGCGCGTACTCTCCGA 2407
QY 2010 AAGCGAGCTGTGGAGCTTTGGCATCTTGTCTCTGGAGACCTTCAGCCTGGGGGCGCTCCCC 2069
Db 2408 AAGCGAGCTGTGGAGCTTTGGCATCTTGTCTCTGGAGACCTTCAGCCTGGGGGCGCTCCCC 2467
QY 2070 CTATCCCAACTCAGCAATCAGCAGACACCGGAGTTTGTGGAGAGGGGGGCGGTCTGCC 2129
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Db 2468 CTATCCCAACTCAGCAATCAGCAGACCGGAGTTTGTGGAGAGGGGGCGGTCTGCC 2527
QY 2130 CTGCCCAGAGCTGTGTCTCTGATCCGCTGTTCCAGGCTCATGGAGCAGTGTCTGGGCTATGA 2189
Db 2528 CTGCCCAGAGCTGTGTCTCTGATCCGCTGTTCCAGGCTCATGGAGCAGTGTCTGGGCTATGA 2587
QY 2190 GCTGGGAGCGGCCCGAGCTTTCAGCACCATCTTACCAGGAGCTGCAGAGCATCCGAAAGCG 2249
Db 2588 GCTGGGAGCGGCCCGAGCTTTCAGCACCATCTTACCAGGAGCTGCAGAGCATCCGAAAGCG 2647
QY 2250 GCATCGG 2256
Db 2648 GCATCGG 2654

RESULT 4
US-10-887-553A-240
; Sequence 240, Application US/10887553A
; Publication No. US20050085436A1
; GENERAL INFORMATION:
; APPLICANT: Garza, Dan
; APPLICANT: Li, Hao
; TITLE OF INVENTION: Method to treat conditions associated
; TITLE OF INVENTION: with insulin signalling dysregulation
; FILE REFERENCE: 4-33262
; CURRENT APPLICATION NUMBER: US/10/887,553A
; PRIOR FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: 60/485,883
; PRIOR FILING DATE: 2003-08-07
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 240
; LENGTH: 2950
; TYPE: DNA
; ORGANISM: human
US-10-887-553A-240

Query Match 14.6%; Score 328.8; DB 21; Length 2950;
Best Local Similarity 62.0%; Pred. No. 1.8e-72;
Matches 573; Conservative 0; Mismatches 342; Indels 9; Gaps 3;

QY 1321 AACCTGTACGACTGGAAGGGGAGGCTTTCCTAGCATTCCTTTGCTCATCGACCACCTA 1380
Db 1918 AACATGTATCGATTTCGAGGGCACTGGGTTTCAAAACATTCCTCAACTTATAGATCATC 1977
QY 1381 CTGAGCACCAGCAGCCCTCCACCAAGAGAGTGGTGTCTCTGCACAGGGTGTGCCCC 1440
Db 1978 TATACAAACAAACAGGTCTATCAAGAAATCAAGGTGTAGTTCTGCTGAATCTCTATTC 2037
QY 1441 AAGGACAAG---TGGGTGTCTGAACCATGAGGACCTGGTGTGGGTGAGCAGATTGGA 1497
Db 2038 AAGGACAAGAAATGGATTCTCAGTCATGAAGATGTATATGGAGAAATTTACTGGGCAAG 2097
QY 1498 GGAACCTTTGGCGAAGTGTTCAGCGACCGCTCGGAGCCGACAAACCCCTGGTGGCGGTG 1557
Db 2098 GGAATTTTGGTGAAGTATATAAGG---GCACATTAAGAGATAAAACTTCTGTGTCTGTT 2154
QY 1558 AAGTCTTGTGAGAGAGCGCTCCACCTGACCTCAAGGCCAAAGTTTCTACAGGAAGCGAGG 1617
Db 2155 AAACATGTAAAGAAAGATCTTCTCAGGAATTTGAAATAAATAATTTTACAGAAAGCCAAA 2214
QY 1618 ATCCTGAAGCAGTACAGCCACCCCAACATCGTGCCTCATTTGGTGTCTGACCCAGAAAG 1677
Db 2215 ATTCTCAAGCAATATGATCATCCCATATTTGTCAAACTTATAGAGTTTGCACACAAAGA 2274
QY 1678 CAGCCCATCTACATCTCATGAGCTTGTGAGGGGGGCGACTTCTGACCTTCTCCCGC 1737
Db 2275 CAGCCTGTCTACATCATATTATGAACTGGTTTTCAGGAGGTGATTTCTCTACCTTCTGAGA 2334
QY 1738 ACGAGGGGGCGCCCTCGGGGTGAAGACTCTCTGTCAGATGGTGGGGGATGAGCTGCT 1797
Db 2335 AGGAAGAGGATGAACCTAAACACTCAAAACAGTTAGTGAATTTTTCATTAGACGCTGCTGCT 2394
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QY 1798 GGATGGAGTACCTGGAGCAAGTCTGCATCCACGGGACCTGGCTCTCGGAAGTCT 1857
Db 2395 GGTATGTTGATCTCGAGAGTAAAACTGTATACACAGGACCTTCTGCAAGAAACTGC 2454
QY 1858 CTGGTGACAGAGAAGAAATGTCCTGAAGATCAGTGAATTTGGGATGTCCCGAGAGGAAGCC 1917
Db 2455 CTGGTAGGTGAAATATATGTTCTGAAATCAGTGAATTTGGGATGTCTGTCAGAGGAT 2514
QY 1918 GATGGGTCTATGACGCTCAGGGGCTCAGCAAGTGTCCCGTGAAGTGGACCGACCT 1977
Db 2515 GGTGGAGTGTATTCATCTTC---TGGCTTAAAGCAGATTCCCATTAATGGACAGCACG 2571
QY 1978 GAGGCTTAACTACGCGCTACTCTCCGAAAGGAGCTGTGGAGCTTTGGCATCTTG 2037
Db 2572 GAAGCTCTTAATATGGAGATACAGTTACAGAGTACAGTGTGGAGCTTTGGCATCTT 2631
QY 2038 CTCTGGGAGACCTTCAGCCTGGGGGCTCCCTTATCCCAACCTCAGCAATCAGCAGCA 2097
Db 2632 CTCTGGGAGACCTTCAGCTTAGGGTTTGTCCGTACCTTGGATGACAAATCAGCAAGCA 2691
QY 2098 CGGAGTTTGGAGAAAGGGGCGCTCTCCCTGCGCAGAGCTGTCTGTATGCGGTG 2157
Db 2692 AGAGAGCAAGTAGAAGAGGATACCGGATGTCTAGCTCCCGACACTGTCCAGAGGATAT 2751
QY 2158 TTCAGGCTCATGGAGCAGTCTGGGCTATGAGCTGGGAGCGGCCAGCTTCAGCAC 2217
Db 2752 TCCAAATCATGATGAAGTGTGGGATATTAACCTGAANAATCGCCCTAAGTTCACTGAA 2811
QY 2218 ATCTACAGGAGCTGCAGACATC 2241
Db 2812 CTTCAGAAAGAGCTCACTATCATC 2835

RESULT 5

US-09-918-995-1503
; Sequence 1503, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hveseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1503
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(449)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-1503

Query Match 14.5%; Score 326.8; DB 10; Length 449;
Best Local Similarity 99.4%; Pred. No. 4.3e-72;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1707 GCAGGGGGGACATTCCTGACCTTCCTCCGACAGGGGGGCGCCCTGGGGGTGAAGAC 1766
Db 120 GCGAGGGGGGACATTCCTGACCTTCCTCCGACAGGGGGGCGCCCTGGGGGTGAAGAC 179
QY 1767 TCTGCTCAGATGTGGGGATGACGTGTCTGGCATGGAGTACCTGGAGACCAAGTCTG 1826
Db 180 TCTGCTCAGATGTGGGGATGACGTGTCTGGCATGGAGTACCTGGAGACCAAGTCTG 239
QY 1827 CATCCCGGACCTGGCTCGGAATCTCGTGCACAGAGAAATGTTCCTGAAGAT 1886

Db 240 CATCCACCGGACCTGGCTCGGAATGCTCGGATGCTGCTGACAGAGAAATGTCTGAAGAT 299
QY 1887 CAGTCACTTTGGGATGTCCTCGAGAGAAAGCCGATGGGTCTATGACGCTCAGGGGGCT 1946
Db 300 CAGTCACTTTGGGATGTCCTCGAGAGAAAGCCGATGGGTCTATGACGCTCAGGGGGCT 359
QY 1947 CAGACAAGTCCCGTGAAGTGGACCGCACCTGAGGCCCTTAACTACGGCCGCTACTCCTC 2006
Db 360 CAGACAAGTCCCGTGAAGTGGACCGCACCTGAGGCCCTTAACTACGGCCGCTACTCCTC 419
QY 2007 CGAAAGCAGCTGTGGAGCTTTGGCATCTT 2036
Db 420 CGAAAGCAGCTGTGGAGCTTTGGCATCTT 449

RESULT 6

US-09-948-802-5
; Sequence 5, Application US/09948802
; Publication No. US20020172981A1
; GENERAL INFORMATION:
; APPLICANT: ROBISON, KEITH E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; FILE REFERENCE: MN1-090
; CURRENT APPLICATION NUMBER: US/09/948,802
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 09/387,212
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 361
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: All occurrences of n indicate any nucleotide
US-09-948-802-5

Query Match 13.1%; Score 296.2; DB 9; Length 361;
Best Local Similarity 97.4%; Pred. No. 2e-64;
Matches 333; Conservative 0; Mismatches 4; Indels 5; Gaps 3;
QY 1613 CGAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGGTCTCATTTGGTCTGCACCC 1672
Db 20 CNAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGGTCTCATTTGGTCTGCACCC 79
QY 1673 AGAAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGCGACTTCTCTGACCTTCC 1732
Db 80 AGAAGCAGCCCATCTACATCGTCATGGAGCTTGTGCAGGGGGCGACTTCTCTGACCTTCC 139
QY 1733 TCCGACGAGGGGGCGCCCTCGGGTGAAGACTCTGTGCAGATGGTGGGGATGCAG 1792
Db 140 TCCGACGAGGGGGCGCCCTCGGGTGAAGACTCTGTGCAGATGGTGGGGATGCAG 199
QY 1793 CTGCTGGCATGAGTACCTGGAGAGCAAGTGTGCATCCACCGGACCTGGCTGCTCGGA 1852
Db 200 CTGCTGGCATGAGTACCTGGAGAGCAAGTGTGCATCCACCGGACCTGGCTGCTCGGA 259
QY 1853 ACTGCTGCTGACAGAGAAGAAATGTCTCTGAAG-ATCAGTGACTTTT-GGGATGTCCGAGA 1910
Db 260 ACTGCTGCTGACAGAGAAGAAATGTCTCTGAAGAAATCAGTGACTTTTGGGATGTCCCAG 319
QY 1911 GGAAGCC---GATGGGTCTATGACGCTCAGGGGCTCAG 1949
Db 320 GGAAGCCGATTTGGGGTCTATGACGCTCAGGGGCTCAG 361

RESULT 7

US-10-121-925-5
; Sequence 5, Application US/10121925
; Publication No. US20030104505A1
; GENERAL INFORMATION:
; APPLICANT: ROBISON, KEITH E.

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
; FILE REFERENCE: MNI-090

; CURRENT APPLICATION NUMBER: US/10/121.925

; CURRENT FILING DATE: 2002-04-12

; PRIOR APPLICATION NUMBER: US/09/948,802

; PRIOR FILING DATE: 2001-09-07

; PRIOR APPLICATION NUMBER: 09/387,212

; PRIOR FILING DATE: 1999-08-31

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 361

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: All occurrences of n indicate any nucleotide

US-10-121-925-5

Query Match 13.1%; Score 296.2; DB 15; Length 361;
Best Local Similarity 97.4%; Pred. No. 2e-64;
Matches 333; Conservative 0; Mismatches 4; Indels 5; Gaps 3;

Qy 1613 CGAGGATCCTGACAGCAGTACATCGTCTGAGGAGTGTGCGTCTGCTGCTGCGACCC 1672

Db 20 CNAAGATCCTGAGAGCAGTACAGCCACCCCAACATCGTGTCTCATTTGGTGTGCGACCC 79

Qy 1673 AGAAGCAGCCCATCTACATCGTCTGAGGAGTGTGCGAGGGGGGCGACTTCTGACCTTCC 1732

Db 80 AGAAGCAGCCCATCTACATCGTCTGAGGAGTGTGCGAGGGGGGCGACTTCTGACCTTCC 139

Qy 1733 TCCGACGAGGGGGCCCGCTGCGGTGAAGACTTGTGTCAGATGCTGGGGGATGCAG 1792

Db 140 TCCGACGAGGGGGCCCGCTGCGGTGAAGACTTGTGTCAGATGCTGGGGGATGCAG 199

Qy 1793 CTGCTGCGATGGAGTACTCGAGAGCAAGTCTGCTGATCCACCGGACCTGGCTGCTCGGA 1852

Db 200 CTGCTGCGATGGAGTACTCGAGAGCAAGTCTGCTGATCCACCGGACCTGGCTGCTCGGA 259

Qy 1853 ACTGCTGCTGACAGAGAGATGCTCTGAAG-ATCAGTGACTTTT-GGGATGTCCCGAGA 1910

Db 260 ACTGCTGCTGACAGAGAGATGCTCTGAAGATCAGTGACTTTTGGGGATGTCCCGAGA 319

Qy 1911 GGAAGCC---GATGGGCTTATGACGCTCAGGGGGCTCAG 1949

Db 320 GGAAGCCGATTTGGGGCTTATGACGCTCAGGGGGCTCAG 361

RESULT 8

US-10-280-576-19

; Sequence 19, Application US/10280576

; Publication No. US2004004405A1

; GENERAL INFORMATION:

; APPLICANT: Woloff, Matthew R.

; TITLE OF INVENTION: VASCULAR STENT OR GRAFT COATED OR IMPREGNATED WITH PROTEIN

; FILE REFERENCE: 09820.189

; CURRENT APPLICATION NUMBER: US/10/280,576

; CURRENT FILING DATE: 2002-10-22

; PRIOR APPLICATION NUMBER: 60/343,732

; PRIOR FILING DATE: 2001-10-25

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 19

; LENGTH: 1779

; TYPE: DNA

; ORGANISM: Drosophila melanogaster

US-10-280-576-19

Query Match 12.0%; Score 271.6; DB 18; Length 1779;

Best Local Similarity 57.0%; Pred. No. 4e-58;

Matches 518; Conservative 0; Mismatches 384; Indels 6; Gaps 1;

Qy 1327 TACCGACTGGAAGGGAGGCTTTCTTCTAGCATTTCTTTGCTCATCGACCACCTACTGAGC 1386

RESULT 9

US-10-003-295-3

; Sequence 3, Application US/10003295

; Publication No. US20020168741A1

; GENERAL INFORMATION:

; APPLICANT: GAN, Weinui et al.

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

Db 844 TTCGGTTCAGGGGACACCAATTTGCCAGCATCCAGAGCTGATGTCATCATGATCATC 903

Qy 1387 ACCCAGCAGCCCTCACCAGAGAGTGGTGTCTCTGCACAGGGGTGTGCCCAAGGAC 1446

Db 904 TCGGAATTCGCACTGACCGTGAATCGGAGCCATATCTCCGACGCCGTTCGCGGAG 963

Qy 1447 AAGTGGTGTGAACCATGAGACCTGGTGTGGTGTGAGCAGATTGAGACGGGGAACTTT 1506

Db 964 CGCTGGGAGCTGAGCAACGATGATGCTGCTGAGAGGATTTGTCGGGGAACTTT 1023

Qy 1507 GCGAAGTGTTCAGCGGAGCCCTGCCAGCGCAACACCTGCTGGTGGGTGAGTCTTGT 1566

Db 1024 GGGGATGTCTACAAGGCCAAACTGAAAGTCCACCAACTGGATGTGGTGTCAAAACCTGT 1083

Qy 1567 CGAGAGACGCTCCCACTGACCTCAAGGCCAAGTTCCTACAGGAAGCAGGATCTCTGAAG 1626

Db 1084 CGAATGACCTGCCCGACGACAGAGCGTAATTCCTACAGGAAGGCCGCACTCTCAAG 1143

Qy 1627 CAGTACAGCACCCCAACATCGTGTCTCATTTGGTGTGTGACACCCAGAAAGACGCCATC 1686

Db 1144 CAATACGATCATCAAAATATCGTAAATTTGATTTGGCATTTGTGTGAGAGAGGCCCATC 1203

Qy 1687 TACATCGTATGAGCTTTGTGAGGGGGGGGACTTCTGACCTTCTCCGACGGGGG 1746

Db 1204 ATGATTTGTATGGAATTTGGTGTCTGCTGCTGCTTTTAACTTTATTACGCAAGAACTCC 1263

Qy 1747 GCCCGCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAGTGTGCGATGGAG 1806

Db 1264 AATGGCTTACCACCTGCCCAACAAATGGGCATGTGCAGAGATGCGGGGAGCGATGCGA 1323

Qy 1807 TACCTCGAGAGCAAGTGTGTCATCCACCGGACCTGGTGTCTCGGAACTGCTGTGGTGA 1866

Db 1324 TATCTGGAGTCCAAAAAATGCAATTCATCGCATCTGCGCGCGGTAAATTTGCTCGTTGAC 1383

Qy 1867 GAGAAAGTCTCTGAAGATCAGTGACTTTGGGATGTCCGAGAGGAGCGGATGGGGTC 1926

Db 1384 TTGGAGCAGAGTGTGAAGATCTCCGATTTGGGAATGTCTCGCGAGGAA-----GAGGAA 1437

Qy 1927 TATGAGCCTCAGGGGGCTCAGCAAGTCCCGTGAAGTGGACCGCACCTGAGGCCCTT 1986

Db 1438 TATATAGTTTCCGATGGCATGAAACAAATACCTGTGAGTGGACAGCTCCCGAGGCCCTG 1497

Qy 1987 AACTACGGCGCTTATCTCTCCGAAAGCAGTGTGGAGCTTTGGCATTTTGTCTTGGGAG 2046

Db 1498 AATTCGGCAAGTACACTTCTGTTGTCGATGTGCTGCTATGTCATGATGTTGGGAG 1557

Qy 2047 ACCTTCAGCTGGGGGCTCCCTCTATCCCACTCAGCATCAGCATCAGCAGACCGGAGTTT 2106

Db 1558 ATCTTCTCAAGGGCGACACACCTTACTCCGGCATGACCAACTCCAGAGCCAGAGAGCGC 1617

Qy 2107 GTGGAGAAGGGGGCGCTGCTGCCCTGCCAGAGCTGTGCTCTGATGCGGTGTTTCCAGGCTC 2166

Db 1618 ATCGATACGGGATATCGTATGCCAACCGCGAGAGCAGCCCGGAGAGATGTACCGACTG 1677

Qy 2167 ATGAGCAGTGTGGGCGCTATGAGCTTGGGAGCGGCCCGGCTTTCAGCACCATCTACCAG 2226

Db 1678 ATGCTCCAGTGTGGGCGAGCGCGAATCCCGACCGCATTTTCGATGATGATCTACAAT 1737

Qy 2227 GAGCTGCA 2234

Db 1738 GTGGTGA 1745

```
; FILE REFERENCE: CL001183DIV
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15297
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-003-295-3

Query Match      10.1%; Score 227.2; DB 13; Length 15297;
Best Local Similarity 71.1%; Pred. No. 7.9e-47;
Matches 394; Conservative 0; Mismatches 8; Indels 152; Gaps 1;

QY 1 ATGGGCTTCTCTCTGAGCTGTGACGCCGCCAGGGCCACGGGGTCTGCGACCAATGCAG 60
Db |||||
QY 61 GAGCCGAGCTTCGTCTACTGAGGGCATGAGAAAGTGGATGGCCAGCGGGTCAAGAGT 120
Db |||||
QY 2563 ATGGGCTTCTCTCTGAGCTGTGACGCCGCCAGGGCCACGGGGTCTGCGACCAATGCAG 2622
Db |||||
QY 61 GAGCCGAGCTTCGTCTACTGAGGGCATGAGAAAGTGGATGGCCAGCGGGTCAAGAGT 120
Db |||||
QY 2563 ATGGGCTTCTCTCTGAGCTGTGACGCCGCCAGGGCCACGGGGTCTGCGACCAATGCAG 2622
Db |||||
QY 121 GACAGGAGTATGACGAGCTGTCTTACACATGTCTCCCTGACGACAGTGGGGCCAGAGC 180
Db |||||
QY 2563 GACAGGAGTATGACGAGCTGTCTTACACATGTCTCCCTGACGACAGTGGGGCCAGAGC 2742
Db |||||
QY 181 CGGGCCATCAGCCCTGACAGCCCATCAGTC----- 211
Db |||||
QY 2743 CGGGCCATCAGCCCTGACAGCCCATCAGTCAGTGGGGTCTCTATGGGACTCTGGTGGGT 2802
Db |||||
QY 212 ----- 211
Db |||||
QY 2803 GCTGGGCTATCTGCCCTTCTCCTTCTCTCTGGGGGCCCTCTGGGGCAGTGGCTGGAGAT 2862
Db |||||
QY 212 ----- 211
Db |||||
QY 2863 CTGGCAGGCAATGCTTGGAGCCATTGTGCCCCCTCTCCCTGCCCTCTCTGTGCTG 2922
Db |||||
QY 212 ---AGTCCTGGGCTGAGATCACCAGCCAACTGAGGGCCCTGAGCCGCTTGTCTGGCGCAGC 268
Db |||||
QY 2923 TATAGTCTGGGCTGAGATCACCAGCCAACTGAGGGCCCTGAGCCGCTTGTCTGGCGCAGC 2982
Db |||||
QY 269 ACCGAGGATCTGAATCTAGGCGCCCTGAGCAAGCTGAGCTGTCTATCCGGGAACGCG 328
Db |||||
QY 2983 ACCGAGGATCTGAATCTAGGCGCCCTGAGCAAGCTGAGCTGTCTATCCGGGAACGCG 3042
Db |||||
QY 329 AGCAGCTTCGCAAGACTTACAGCGAGCAGTGGCGAGCTGCGAGGAGCTCACCAGA 388
Db |||||
QY 3043 AGCAGCTTCGCAAGACTTACAGCGAGCAGTGGCGAGCTGCGAGGAGCTCACCAGA 3102
Db |||||
QY 389 CCCACAGCCAGGAC 402
Db |||||
QY 3103 TGAGCGGCGAGCAC 3116
Db |||||

RESULT 11
US-10-101-510-525
; Sequence 525, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 525
; LENGTH: 3875
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-525

Query Match      8.9%; Score 201.2; DB 15; Length 3875;
Best Local Similarity 54.9%; Pred. No. 2.2e-40;
Matches 423; Conservative 0; Mismatches 338; Indels 9; Gaps 1;
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1511	Qy	1451	GGGTGCTGAACCATGAGCACTGGTGTGGTGTGACAGATGTGACGGGGGAACCTTTGGCG	1510
1969	Db	1969	GGGAGCTTGATCCAGCGTGGCTGATGGTGACACTGTCTATAGGAGAAAGSAGAGATTTGGGG	2028
1511	Qy	1511	AAGTGTTCAGCGGACGCTCGAGCC-----GACAAACCCCTGGTGGCGGTGAAGT	1561
2029	Db	2029	AAGTGTATCGAGGACCCCTGAGGCTCCCAGCCNGGACTCGAAGACTGTGGCCATTAAGA	2088
1562	Qy	1562	CTTGTCTGAGAGAGCGCTCCCACTGACCTCAAGGCCAAAGTTTCTACAGGAAGCGAGGATCC	1621
2089	Db	2089	CCTTAAAGACACATCCCCAGGTGGCCAGTGGTGGAACTTCTTCGAGAGGCAACTATCA	2148
1622	Qy	1622	TGAAGCACTACAGCCACCCCAACATCGTGGCTCTCATTTGGTGTCTGACCCAGACGACG	1681
2149	Db	2149	TGGGCCAGTTTAGCCACCCGCATATCTGCATCTGGAAGGCGTCGTACAAAAGCGAAAGC	2208
1682	Qy	1682	CCATCTACATCGTCATGGAGCTGTGCAGGGGGGCGACTTCCTGACCTTCCTCCGCAACGG	1741
2209	Db	2209	CGATCATGATCNTACAGAAATTTATGGAGAAATGGAGCCCTGGATGCTTCTTGAGGGAGC	2268
1742	Qy	1742	AGGGGGCCCCCTGCGGGTGAAGACTCTGCTGCAGATGGTGGGGATGCAAGCTGCTGGCA	1801
2269	Db	2269	GGGAGGACCAAGCTGGTCCCTGGGCAGCTAGTGGCCATGCTCGAGGGCATAGCATCTGGCA	2328
1802	Qy	1802	TGGAGTACCTGGAGAGCAAGTGTGCATCACCGGGACCTGGCTGCTCGGAACGTCCTGG	1861
2329	Db	2329	TGAACCTCCTCAGTAATACAAATTTATGTCCACCGGGACCTGGCTGCCAGAAAACATCTTGG	2388
1862	Qy	1862	TGACAGAGAAGATGTCTCGAAGATCAGTCAGCTTTGGGATGTCCGAGAGGAAGCCGATG	1921
2389	Db	2389	TGAATCAAACCTGTGCTGCAAGGTGTCTGACTTTTGGCCTGACTCGCCTCTCGATGACT	2448
1922	Qy	1922	GGGTCTATGCAAGCCTCAGGGGGCCTCAGACAAGTCCCGTGAAGTGGACCGCACCTGAGG	1981
2449	Db	2449	TTGATGCCACATACGAACCCAGGGAGGAAGATCCCTATCCGTGGACAGCCCCGGAAG	2508
1982	Qy	1982	CCCTTAATACGGCCGTACTCTCCGAAAGACGACGTGTGAGGCTTTGGGCACTTGTGCTCT	2041
2509	Db	2509	CCATTGCCCATCGGATCTTACCACAGCCAGCGATGTGTGGAGCTTTGGGATTTGTGATGT	2568
2042	Qy	2042	GGGAGACCTTCAGCTGGGGGCGCTCCCCCTATCCCAACCTCAGCAATCAGCACACAGCGG	2101
2569	Db	2569	GGGAGGTGCTGAGCTTTTGGGGAAGAAGCTTTATGGGGAGATGAGCAATCAGAGGTTATGA	2628
2102	Qy	2102	AGTTTGTGGAGAAGGGGGCGCTGTGCCCTGCCAGAGCTGTGTCTGTGATGCCGTGTTC	2161
2629	Db	2629	AGAGCATTGAGGATGGGTACCGGTGGCCCTCTCTGTGGACTGCCCTGCCCTCTGTATG	2688
2162	Qy	2162	GGCTCTGAGAGCACTGTGGGCCCTATGAGCCTGGGCAAGCGGCCAGCTTC	2211
2689	Db	2689	AGTTCATGAAGAACTGTGGGCAATATGACCGTGGCCGTGCCCGGCCCAACATCTTC	2738

RESULT 12

US-10-384-339C-1
Sequence 1, Application US/10384339C
Publication No. US20040175703A1
GENERAL INFORMATION:
APPLICANT: Kreutzer, Roland
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GENE
CURRENT APPLICATION NUMBER: US/10/384,339C
CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: PCT/EP02/00152
PRIOR FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: DE 10100586.5
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: DE 10155280.7
PRIOR FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: DE 10158411.3
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: DE 10160151.4
PRIOR FILING DATE: 2001-12-07

RESULT 13
US-09-967-768A-144
; Sequence 144, Application US/09967768A
; Patent No. US20020150877A1
; GENERAL INFORMATION:

APPLICANT: Augustus, Meena
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-72
CURRENT APPLICATION NUMBER: US/09/967,768A
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/60/236,109
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,034
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,111
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 325
SOFTWARE: PatentIn version 3.0
SEQ ID NO 144
LENGTH: 3370
TYPE: DNA
ORGANISM: Homo sapiens
US-09-967-768A-144

Query Match 8.8%; Score 198; DB 9; Length 3370;
Best Local Similarity 54.7%; Pred. No. 1.4e-39;
Matches 421; Conservative 0; Mismatches 340; Indels 9; Gaps 1;
QY 1451 GGGTCTGAACCATGAGACCTGGTGTGGTGAAGAGATTGGACGGGAACTTTGGCG 1510
DB 1967 GGGAGCTTGATCCAGCGTGGCTGATGTGGGACACTGTCTATAGGAGAGAGATTGGGG 2026
QY 1511 AAGTGTTCAGCGGACCTCGCGAGCC-----GACAACACCTGGTGGCGGTGAAGT 1561
DB 2027 AAGTGTATCGAGGACCTTCAGGCTCCCGACGAGGACTGCAAGACTGTGGCCATTAGA 2086
QY 1562 CTGTGAGAGACCTCCCACTGACCTCAAGGCCAAAGTTTCTACAGGAAGCGAGGATCC 1621
DB 2087 CCTTAAAGACACATCCCGAGGTGCCAGTGGTGAAGTCTCTTCGAGAGCAACTATCA 2146
QY 1622 TGAAGCAGTACAGCCACCCCAACATCTGCTGCTCATTTGTGTCTGCACCAGAACGAC 1681
DB 2147 TGGCCAGTTAGCCACCCCGATATCTGCTATCTGGAAGCGTCGTCAAAAGCGAAAGC 2206
QY 1682 CCATCTACATGTCATGAGACTTGTGAGGGGGGCGACTTCTGACCTTCTCCCGACCG 1741
DB 2207 CGATCATGATCATACAGAAATTTATGAGAAATCAGCCCTGGATGCTTCTGAGGGAGC 2266
QY 1742 AGGGGGCCCTCGCGGTGAAGACTCTGCTGAGATGTGGGGGATGAGCTGTGGCA 1801
DB 2267 GGAGAGCAGCTGGTCCCTGGGCGACTAGTGGCCATGCTGCAGGSCATAGCATCTGCA 2326
QY 1802 TGAAGTACTGAGAGCAAGTGTGATCCACCGGACCTGGCTGCTCGGAACCTGCTGG 1861
DB 2327 TGAAGTACTGAGTACCAATATGATCCACCGGACCTGGCTGCGCAAAACATCTTGG 2386
QY 1862 TGACAGAGAGATGCTTGTGAGATCAGTGTGAGTGTGGGATGTCGCGAGAGGAGCCGATG 1921
DB 2387 TGAATCAAAACCTGTGCTCAAGAGTGTGACTTTGGCTGACTCGCTCTCTGGATGACT 2446
QY 1922 GGGTCTATGAGCGCTCAGGGGGCTCAGACAAAGTCCCGTGAAGTGGACCCGACCTGAGG 1981
DB 2447 TTGATGGCACAATCAAGAACCCAGGAGGAAAGATCCCTATCCGTTGGACAGCCCTGAAG 2506
QY 1982 CCCTTAACCTAGCGCGCTACTCTCTCGAAAGCGAGCTGTGGAGCTTTGGCATCTTGTCTCT 2041
DB 2507 CCAATTGCCATCGGATCTTCCACAGCAGCAGCGATGTGTGGAGCTTTGGATTTGTATG 2566
QY 2042 GGGAGACCTTCAGCTGGGGGCTCCCTCTATCCCACTAGCAATCAGAGAGACAGGG 2101
DB 2567 GGGAGGTGCTAGCTTTGGGGACAAGCTTATGGGGAGATGAGCAATCAGAGAGTTATGA 2626
QY 2102 AGTTTGTGAGAGGGGGCGCTGTGCCCCGAGAGCTGTGCTGCTGATCCGCTGTTCATCA 2161
DB 2627 AGAGCATTTGAGGATGGGTACCGTTTGGCCCCCTCTCTGTGGAATGCGCTGCCCCCTCTG 2686
QY 2162 GGCTCATGAGCAGTGTCTGGGCTTATGAGCTTGGGACCGGCCCGACCTTC 2211

DB 2687 AGCTCATGAAGAAGTGTGGCATATGACCGTCCCGCGCCACACACTTC 2736
RESULT 14
US-10-354-358-101
Sequence 101, Application US/10354358
Publication No. US20030157082A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc
APPLICANT: Hunter, John Joseph
APPLICANT: MacBeth, Kyle J.
APPLICANT: Teal, Fong-Ying
APPLICANT: Lesoon, Andrea
APPLICANT: Lightcap, Eric S.
APPLICANT: Williamson, Mark
APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
TITLE OF INVENTION: 3703, 14171, 10359, 15660, 1450, 18894, 2088, 32427, 2160,
TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
TITLE OF INVENTION: 16334, 68862, 9011, 14031, 5178, 21225, 1420, 32236, 2099,
FILE REFERENCE: MPT02-020FIRMNMIM
CURRENT APPLICATION NUMBER: US/10/354,358
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: US 60/353,600
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 60/364,517
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/371,075
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: US 60/371,507
PRIOR FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: US 60/372,984
PRIOR FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: US 60/374,194
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/382,995
PRIOR FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 60/385,023
PRIOR FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: US 60/388,853
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 60/389,395
PRIOR FILING DATE: 2002-06-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 101
LENGTH: 3370
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (94)...(3048)
US-10-354-358-101

Query Match 8.8%; Score 198; DB 16; Length 3370;
Best Local Similarity 54.7%; Pred. No. 1.4e-39;
Matches 421; Conservative 0; Mismatches 340; Indels 9; Gaps 1;
QY 1451 GGGTCTGAACCATGAGGACCTGGTGTGGTGAAGAGATTGGACGGGAACTTTGGCG 1510
DB 1967 GGGAGCTTGATCCAGCGTGGCTGATGTGGGACACTGTCTATAGGAGAGAGATTGGGG 2026
QY 1511 AAGTGTTCAGCGGACCGCTGCGAGCC-----GACAACACCTGGTGGCGGTGAAGT 1561
DB 2027 AAGTGTATGAGGAGACCTTCAGGCTCCCGACGAGGACTGTGGCCATTAGA 2086
QY 1562 CTGTGAGAGAGCGTCCCGACCTGACCTCAAGCCCAAGTTTCTACAGGAGGAGGATCC 1621


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Qy 1622 TGAAGCAGTAGACACCCCAACATCGTGGCTCTCATTTGGTGTCTGCACCCAGAAAGCAGC 1681
Db 2147 TGGGCCAGTTTAGCCACCCGCATATTCTGATCTGGAAGGCGTCTGCACAAAGCGAAAGC 2206
Qy 1682 CCATCTACATCGTATGAGACCTTGTGAGGGGGCGACTTCTTGACCTTCTCCGCGACGG 1741
Db 2207 CGATCATGATCATACAGAAATTTATGGAAGTGCAGCCCTGGATGCCCTTCCTGAGGAGC 2266
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Db 2267 GGAGAGACAGCTGGTCCCTGGGAGCTAGTGGCCATGCTGCAGGGCATAGCATCTGGCA 2326
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Qy 1862 TGACAGAGAAGATGCTCTGAAAGATCAGTCTTGGGATGTCCCGAGAGAAAGCGGATG 1921
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; Sequence 19, Application US/10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Rubin, Mark A.
; APPLICANT: Sreekumar, Arun
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; CURRENT APPLICATION NUMBER: US/10/210,120
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 19
; LENGTH: 3370
; TYPE: DNA
; ORGANISM: Homo sapiens
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Best Local Similarity 54.7%; Pred. No. 1.4e-39;
Matches 421; Conservative 0; Mismatches 340; Indels 9; Gaps 1;
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Job time : 2017.27 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2256	100.0	2674	4	US-10-003-295-1
3	296.2	13.1	361	3	US-09-387-212-5
4	296.2	13.1	361	3	US-09-948-802-5
5	227.2	10.1	15297	3	US-09-817-180-3
6	227.2	10.1	15297	4	US-10-003-295-3
7	213	9.4	19152	4	US-09-949-016-12110
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12	174.6	7.7	3386	4	US-09-949-016-5662
13	174.6	7.7	3416	2	US-08-357-642A-2
14	174.6	7.7	3416	2	US-08-460-626-2
15	174.6	7.7	3416	4	US-09-016-434-1483
16	174.6	7.7	4089	4	US-09-300-958A-13
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22	170.4	7.6	2455	4	US-09-949-016-4411
23	169.4	7.5	3623	1	US-08-306-691B-35
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25	169.4	7.5	5763	4	US-09-949-016-3759
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ALIGNMENTS

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US-09-817-180-1

; Sequence 1, Application US/09817180

; Patent No. 6340584

; GENERAL INFORMATION:

; APPLICANT: GAN, Weiniu et al.

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; FILE REFERENCE: CLO01183

; CURRENT APPLICATION NUMBER: US/09/817,180

; CURRENT FILING DATE: 2001-03-27

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 2674

; TYPE: DNA

; ORGANISM: Human

US-09-817-180-1

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Db	72	ATGGGCTTCTTCTGAGCTGTGACGCGCCCGCCAGCGGCTCTGCGAGCAATCGAG	131		
Qy	61	GAGGCCGAGCTTCTGCTTCTGAGGCGCATGAGAAAGTGGATGCCAGCGGCTCAAGAGT	120		
Db	132	GAGGCCGAGCTTCTGCTTCTGAGGCGCATGAGAAAGTGGATGCCAGCGGCTCAAGAGT	191		
Qy	121	GACAGGAGTATCAGAGCTGTCTTCCACATCTCCCTGCAGACAGTGGGGGCCAGAGC	180		
Db	192	GACAGGAGTATCAGAGCTGTCTTCCACATCTCCCTGCAGACAGTGGGGGCCAGAGC	251		
Qy	181	CGGGCCATCAGCCCTGACAGCCCATCAGTCTGCTGGGCTGAGATCAGCGCCCAACT	240		
Db	252	CGGGCCATCAGCCCTGACAGCCCATCAGTCTGCTGGGCTGAGATCAGCGCCCAACT	311		
Qy	241	GAGGGCTGAGCCGCTTGTGCGGCGAGCAGCAGAGATCTGAATCTCAGGGCCCTTGAGC	300		
Db	312	GAGGGCTGAGCCGCTTGTGCGGCGAGCAGCAGAGATCTGAATCTCAGGGCCCTTGAGC	371		
Qy	301	AAGCTGAGCTGTCTATCCGGGAACGGCAGCAGCTTCGCAAGACCTACAGCGAGCTGG	360		
Db	372	AAGCTGAGCTGTCTATCCGGGAACGGCAGCAGCTTCGCAAGACCTACAGCGAGCTGG	431		
Qy	361	CACAGCTGAGGAGCTGATCAGACCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	420		

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DB 1932 GTGACAGAGAAATGTCTTGAAGATCAGTGAATTTTGGGATGTCCCGAGAGGAAGCCGAT 1991
QY 1921 GGGGTCTATGACAGCTCAGGGGGCTCAGACAAAGTCTCCCGAGAGCTTGGGATCTTGGCATCTTGTCTC 2040
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QY 1981 GCGCTTAACTACGCGCGCTACTCTCCGAAAGCAGCTGTGGAGCTTGGGATCTTGGCATCTTGTCTC 2111
DB 2052 GCGCTTAACTACGCGCGCTACTCTCCGAAAGCAGCTGTGGAGCTTGGGATCTTGGCATCTTGTCTC 2100
QY 2041 TGGGAGACTTTCAGGCTGCGGGCTTCCCTTATCCAACTCAGCAATCAGCAGACAGG 2100
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; Sequence 1, Application US/10003295
; Patent No. 6686187
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01183DIV
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-003-295-1

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Qy	301	AAGCTGAGCTTCTATCCGGGAAACGGGAGCAGCTTCGCAAGACCTACGCGAGCTGG	360		
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Db	1392	AACCTGTACCGACTGGAAGGGGAAAGCTTTCTTAGCAATTCCTTTGTCTCATCGACCCTA	1451		
Qy	1381	CTGAGACCCAGAGAGCCCTCACCAGAGAGTGTGTCTCTGACAGGGCTGTGCCC	1440		
Db	1452	CTGAGACCCAGAGAGCCCTCACCAGAGAGTGTGTCTCTGACAGGGCTGTGCCC	1511		
Qy	1441	AAGGACAGTGGGTGTGAAACATGAGGACCTCGTGTGGGTGAGCAGATTTGACGGGG	1500		
Db	1512	AAGGACAGTGGGTGTGAAACATGAGGACCTCGTGTGGGTGAGCAGATTTGACGGGG	1571		
Qy	1501	AACCTTTGGGGAAGTGTTCAGCGGACCCCTGCGAGCCGACAAACCCCTGTGGGGTGAAG	1560		
Db	1572	AACCTTTGGGGAAGTGTTCAGCGGACCCCTGCGAGCCGACAAACCCCTGTGGGGTGAAG	1631		
Qy	1561	TCCTGTGAGAGAGCTTCCCACTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGATC	1620		
Db	1632	TCCTGTGAGAGAGCTTCCCACTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGATC	1691		
Qy	1621	CTGAAGCAGTACAGCCACCCCAACATCTGCTGCTCATTTGGTGTCTGACCCAGAAACGAG	1680		
Db	1692	CTGAAGCAGTACAGCCACCCCAACATCTGCTGCTCATTTGGTGTCTGACCCAGAAACGAG	1751		
Qy	1681	CCCATCTACATCGTCTGAGAGCTTGTGAGGGGGGCGACTTCTGTGACCTTCTCCGACG	1740		
Db	1752	CCCATCTACATCGTCTGAGAGCTTGTGAGGGGGGCGACTTCTGTGACCTTCTCCGACG	1811		
Qy	1741	GAGGGGCGCGCTGCGGGTGAAGACTCTGCTGACATGGTGGGGGATGACGCTGTGCG	1800		
Db	1812	GAGGGGCGCGCTGCGGGTGAAGACTCTGCTGACATGGTGGGGGATGACGCTGTGCG	1871		
Qy	1801	ATGGAGTACTGAGAGCAAGTCTGCATCCACGGGACCTGCTGCTCGGAACTGCTG	1860		
Db	1872	ATGGAGTACTGAGAGCAAGTCTGCATCCACGGGACCTGCTGCTCGGAACTGCTG	1931		
Qy	1861	GTGACAGAGAAGTATCTCTGAAAGATCAGTGAATTTTGGGATGTCCCGAGAGGAAGCCGAT	1920		
Db	1932	GTGACAGAGAAGTATCTCTGAAAGATCAGTGAATTTTGGGATGTCCCGAGAGGAAGCCGAT	1991		
Qy	1921	GGGGTCTATGACGCTCAGGGGCTCAGCAAGTCCCGTGAAGTGGACCGACCTGAG	1980		
Db	1992	GGGGTCTATGACGCTCAGGGGCTCAGCAAGTCCCGTGAAGTGGACCGACCTGAG	2051		
Qy	1981	GCCCTTAACTACGGCGCTACTCTCCGAAAGCGAGTGTGGAGCTTTGGCATCTTGCTC	2040		
Db	2052	GCCCTTAACTACGGCGCTACTCTCCGAAAGCGAGTGTGGAGCTTTGGCATCTTGCTC	2111		
Qy	2041	TGGGAGACCTTACGCTGGGGGCTTCCCTCTATCCCAACCTCAGCAATCAGACAGACGG	2100		
Db	2112	TGGGAGACCTTACGCTGGGGGCTTCCCTCTATCCCAACCTCAGCAATCAGACAGACGG	2171		
Qy	2101	GAGTTTGTGAGAGAGGGGGGCGCTGTGCGCTGCCAGAGCTGTGCTCTGATGCGGTTC	2160		

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Db 2232 AGGCTCATGAGCAGTCTGGGCTATGAGCCTGGCAGCGGCCAGCTTTCAGCACCATC 2291
QY 2221 TACCAGAGCTGCAGAGCATCCGAAAGCGGCATCGG 2256
Db 2292 TACCAGAGCTGCAGAGCATCCGAAAGCGGCATCGG 2327

RESULT 3

US-09-387-212-5
; Sequence 5, Application US/09387212A
; Patent No. 6309849
; GENERAL INFORMATION:
; APPLICANT: ROBISON, KEITH E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
; FILE REFERENCE: MNI-090
; CURRENT APPLICATION NUMBER: US/09/387,212A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 361
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: All occurrences of n indicate any nucleotide
US-09-387-212-5

Query Match 13.1%; Score 296.2; DB 3; Length 361;
Best Local Similarity 97.4%; Pred. No. 6e-56;
Matches 333; Conservative 0; Mismatches 4; Indels 5; Gaps 3;
QY 1613 CGAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGGCTCTCATTTGGTGTCTGCACCC 1672
Db 20 CNAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGGCTCTCATTTGGTGTCTGCACCC 79
QY 1673 AGAAGCAGCCATCTACATCGTCAATGAGCTTGTGAGGGGGCGACTTCTGACCTTCC 1732
Db 80 AGAAGCAGCCATCTACATCGTCAATGAGCTTGTGAGGGGGCGACTTCTGACCTTCC 139
QY 1733 TCCGACGGAGGGGGCCGCTGCGGTGAAGACTCTGCTGCAGATGGTGGGGATGCAG 1792
Db 140 TCCGACGGAGGGGGCCGCTGCGGTGAAGACTCTGCTGCAGATGGTGGGGATGCAG 199
QY 1793 CTGCTGGCATGGAGTACCTGGAGAGCAAGTCTGCATCCACCGGGACCTGGCTGCTCGGA 1852
Db 200 CTGCTGGCATGGAGTACCTGGAGAGCAAGTCTGCATCCACCGGGACCTGGCTGCTCGGA 259
QY 1853 ACTGCTGGTGCAGAGAGAAATGCTCTGAAG-ATCAGTACTTT-GGGATGTCGCGAGA 1910
Db 260 ACTGCTGGTGCAGAGAGAAATGCTCTGAAGAAATCAGTACTTTGGGGATGTCCCGAGA 319
QY 1911 GGAAGCC---GATGGGTCTATGAGCTCAGGGGGCTCAG 1949
Db 320 GGAAGCCGATTGGGGTCTATGAGCTCAGGGGGCTCAG 361

RESULT 4

US-09-948-802-5
; Sequence 5, Application US/09948802
; Patent No. 6465232
; GENERAL INFORMATION:
; APPLICANT: ROBISON, KEITH E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
; FILE REFERENCE: MNI-090
; CURRENT APPLICATION NUMBER: US/09/948,802
; CURRENT FILING DATE: 2001-09-07

; PRIOR APPLICATION NUMBER: 09/387,212
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 361
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: All occurrences of n indicate any nucleotide
US-09-948-802-5

Query Match 13.1%; Score 296.2; DB 3; Length 361;
Best Local Similarity 97.4%; Pred. No. 6e-56;
Matches 333; Conservative 0; Mismatches 4; Indels 5; Gaps 3;
QY 1613 CGAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGGCTCTCATTTGGTGTCTGCACCC 1672
Db 20 CNAGGATCCTGAAGCAGTACAGCCACCCCAACATCGTGGCTCTCATTTGGTGTCTGCACCC 79
QY 1673 AGAAGCAGCCATCTACATCGTCAATGAGCTTGTGAGGGGGCGACTTCTGACCTTCC 1732
Db 80 AGAAGCAGCCATCTACATCGTCAATGAGCTTGTGAGGGGGCGACTTCTGACCTTCC 139
QY 1733 TCCGACGGAGGGGGCCGCTGCGGTGAAGACTCTGCTGCAGATGGTGGGGATGCAG 1792
Db 140 TCCGACGGAGGGGGCCGCTGCGGTGAAGACTCTGCTGCAGATGGTGGGGATGCAG 199
QY 1793 CTGCTGGCATGGAGTACCTGGAGAGCAAGTCTGCATCCACCGGGACCTGGCTGCTCGGA 1852
Db 200 CTGCTGGCATGGAGTACCTGGAGAGCAAGTCTGCATCCACCGGGACCTGGCTGCTCGGA 259
QY 1853 ACTGCTGGTGCAGAGAGAAATGCTCTGAAG-ATCAGTACTTT-GGGATGTCGCGAGA 1910
Db 260 ACTGCTGGTGCAGAGAGAAATGCTCTGAAGAAATCAGTACTTTGGGGATGTCCCGAGA 319
QY 1911 GGAAGCC---GATGGGTCTATGAGCTCAGGGGGCTCAG 1949
Db 320 GGAAGCCGATTGGGGTCTATGAGCTCAGGGGGCTCAG 361

RESULT 5

US-09-817-180-3
; Sequence 3, Application US/09817180
; Patent No. 6340584
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001183
; CURRENT FILING DATE: 2001-03-27
; CURRENT APPLICATION NUMBER: US/09/817,180
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15297
; TYPE: DNA
; ORGANISM: Human
US-09-817-180-3

Query Match 10.1%; Score 227.2; DB 3; Length 15297;
Best Local Similarity 71.1%; Pred. No. 3.1e-40;
Matches 394; Conservative 0; Mismatches 8; Indels 152; Gaps 1;
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Db 2563 ATGGGGCTTCTTCTCTGAGCTGTGCAGCCCGCCAGGGGTCTCTGAGCAAAATGCAG 2622
QY 61 GAGGCCGAGCTTCTCTTACTTCTGAGGGCATGAGAAATGATGATGCCAGCGGGTCAAGAT 120
Db 2623 GAGGCCGAGCTTCTCTTACTTCTGAGGGCATGAGAAATGATGATGCCAGCGGGTCAAGAT 2682

[illegible]

/	PRIOR APPLICATION NUMBER:	60/237,768
/	PRIOR FILING DATE:	2000-10-03
/	PRIOR APPLICATION NUMBER:	60/231,498
/	PRIOR FILING DATE:	2000-09-08
/	NUMBER OF SEQ ID NOS:	207012
/	SOFTWARE:	PastSeq for Windows Version 4.0
/	SEQ ID NO	5662
/	LENGTH:	3386
/	TYPE:	DNA
/	ORGANISM:	Human
/	US-09-949-016-5662	
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Matches 392; Conservative 0; Mismatches 319; Indels 6; Gaps 2;		
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Db	1386	GGGGAGGTCTATGAAGGTGCTTACACAATATCAAAAGGGGAGAATAATCATGTAGCTGTC 1445
Qy	1558	AAGTCTTTGTCGAGACGCCTCCACACTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGG 1617
Db	1446	AAGACTGCAAGAAAGNCTGCACTCTGGAACAACAAGGAGAAGTTTCATGACGGAGCAGTG 1505
Qy	1618	ATCCTGAAGCAGTACAGCCACCCCAAACATCGTGGCTCTCATTTGGTGTCGACCCCAAG 1677
Db	1506	ATCATGAAGAACCTCGACCACCCGCACATCGTGAAGCTGATCGGCAT--CAATTGAAGAG 1562
Qy	1678	CAGCCCATCTACATCGTATGAGACTTGTGCAGGGGGGCACCTCTCTGACCTTTCCTCCGC 1737
Db	1563	GAGCCCCACCTGGGATCATCATGGTAATTGTATCCCTATGGGAGCTGGGCCACTACCTGGAG 1622
Qy	1738	ACGAGGGGGCCCGCCTCGGGTGAAGACTCTGCTGCAGATGTTGGGGGATGCAGCTGCT 1797
Db	1623	CGGAAACAAGAACTCCCTGAAGTGCTCACCTCGTGTGTACTCACTGCAGATATGCAAA 1682
Qy	1798	GGCATGGAGTACCTGGAGACAAAGTGTGTGATCCACGGGACCTGGCTGTGCGAACTGC 1857
Db	1683	GCCATGSCCTACCTGGAGAGCATCAACTGGGTGCACAGGGACATTTGCTGCCGAAACATC 1742
Qy	1858	CTGGTGCACAGAGAAGATGTCCTGAAGATCAGTGACTTTGGGATGTCGCCGAGGAGGCC 1917
Db	1743	CTGGTGGCTCCCCTGAGTGTGTGAAGCTGGGGACTTTGGTCTTCCCGGTACATTGAG 1802
Qy	1918	GATGGGTCTATGCAGCTCAGGGGGCTCAGACAAGTCCCGTGAAGTGGACCGCACCT 1977
Db	1803	GACGAGACTAT---TACAAGACCTCTGTGACTGCTCTCCCAATCAATGGATGCCCA 1859
Qy	1978	GAGGCCCTTAACCTACGGCCGCTACTCTCCGAAAGCAGCTGTGGAGCTTTGGCATCTTG 2037
Db	1860	GAGTCCATTAACTTTCGACGCTTCACGACAGCCAGTAGCAGCTGTGGATGTTCCGCGTGTG 1919
Qy	2038	CTTGGGAGACTTCAGCCTGGGGCCCTCCCCCTATCCCAACCTCAGCAATCAGCAGACA 2097
Db	1920	ATGTGGGAGATCTCTGAGCTTTGGGAAGCAGCCCTTCTTCTGGCTGGAGAACAAAGGATGTC 1979
Qy	2098	CGGAGATTGTGGAGAAAGGGGGCCGCTGCCTCCCGCCAGAGCTGTGCTCTGATGCCGTG 2157
Db	1980	ATCGGGGTGCTGGAGAAAGGNAGACGGCTGCCCAAGCTGATCTCTGTCCACCGTCTTT 2039
Qy	2158	TTCAGGCTCATGGAGCAGTGTCTGGGCCCTATGAGCTGGGACGCGGCCAGCTTCAGC 2214
Db	2040	TATACCTCTATGACCCGCTGCTGGACTATGAGCCCTCAGTGAACGGGCCCCGCTTCACC 2096

TITLE OF INVENTION: AND METHODS
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/357,642A
 FILING DATE: December 15, 1994
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 209/070
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3416
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: nucleic
 US-08-357-642A-2

APPLICANT: Joseph Schlessinger
TITLE OF INVENTION: PYK2 RELATED PRODUCTS

Search completed: August 9, 2005, 21:35:06
Job time : 502.791 secs

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1483:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3416 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 5988304
; US-09-016-434-1483

Query Match          7.7%; Score 174.6; DB 4; Length 3416;
Best Local Similarity 54.7%; Pred. No. 7.5e-29;
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QY 1476 AAGACCTGCAAGAAGACTGCACTCTGGACAACAAGGAGAAGTTTCATGAGCGAGGCGAGTG 1535
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QY 1618 ATCTGAAGCAGTACAGCCACCCCAACATCGTGGCTCTCATTTGGTCTTGCACCCAGAAAG 1677
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1536 ATCATGAAGAACCTCGACCAACCCGACATCGTGAAGCTGATCGGCAT---CATTGAAGAG 1592
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1678 CAGCCCATCTACATCGTCATGGAGCTGTGACGGGGGGGACCTTCTGACCTTCTCTCCGC 1737
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 1738 ACGAGGGGCGCGCTGCGGGTGAAGACTCTCTGCAGATGGTGGGGATGCAGCTGCT 1797
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QY 1773 CTGTTGGCTCTCCCTGAGTGTGTGAAGCTGGGGGACTTTTGGTCTTTCCCGGTACATTGAG 1832
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QY 1918 GATGGGCTCTATGAGCCTCAGGGGGCCTCAGACAAGTCCCCGTGAAGTGGACCCGACCT 1977
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DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 1890 GAGTCCATTAACTTCGACGCTTTCACGACAGCAGTGAOCTCTGGATGTTTCGCCGTGTC 1949
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QY 2038 CTCTGGGAGACCTTCAGCCTGGGGGCTCCCCCTATCCCAACCTCAGCAATCAGCAGACA 2097
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1950 ATGTGGAGATCTTGAGCTTTGGAGACGACCCCTTCTTCTGGCTGGAGAACAGGATGTC 2009
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2098 CGGAGTGTGTGGAGAAAGGGGGCCGTCTCCCTGCCCCAGAGCTGTGTCTGTATGCCGTG 2157
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2010 ATCGGGGTGTGGAGAAAGGAGACCGGCTGCCCAAGCCTGATCTCTGTCCACCGGTCCIT 2069
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QY 2158 TTCAAGCTCATGAGCAGTGTGGCCCTATGAGCTGGGCGGAGCGGCCCGCTTCAGC 2214
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QY 2070 TATACCTCATGACCCGCTGTGGGACTACGACCCCAAGTACCGGCCCGCCCTTCACC 2126
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GenCore version 5.1.6
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27: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2674	100.0	2674	18	US-10-660-763-1
3	2326.4	87.0	2889	16	US-10-240-965-256
4	362.4	13.6	15297	13	US-10-003-295-3
5	362.4	13.6	15297	18	US-10-660-763-3
6	328.8	12.3	2950	21	US-10-887-553A-240
7	326.8	12.2	449	10	US-09-918-995-1503

296.2	11.1	361	9	US-09-948-802-5	Sequence 5, Appli
296.2	11.1	361	15	US-10-121-925-5	Sequence 5, Appli
271.6	10.2	1779	18	US-10-280-576-19	Sequence 19, Appl
201.2	7.5	3875	15	US-10-101-510-525	Sequence 525, App
198	7.4	2955	19	US-10-384-339C-1	Sequence 1, Appli
198	7.4	3370	9	US-09-967-768A-144	Sequence 144, App
198	7.4	3370	16	US-10-354-358-101	Sequence 101, App
198	7.4	3370	16	US-10-210-120-19	Sequence 19, Appl
198	7.4	3370	19	US-10-776-827-82	Sequence 82, Appl
198	7.4	3370	20	US-10-473-974-219	Sequence 219, App
198	7.4	3370	21	US-10-843-641A-6289	Sequence 6289, Ap
198	7.4	3370	22	US-10-909-035-19	Sequence 19, Appl
185.4	6.9	3042	19	US-10-384-339C-2	Sequence 29, Appl
185.4	6.9	3921	10	US-09-921-406C-29	Sequence 222, App
185.4	6.9	3921	15	US-10-007-926A-22	Sequence 19, Appl
185.4	6.9	3921	16	US-10-269-909-19	Sequence 1, Appli
185.4	6.9	3921	17	US-10-366-288-1	Sequence 1, Appli
185.4	6.9	3921	17	US-10-172-118-1036	Sequence 1036, Ap
185.4	6.9	3921	18	US-10-342-887-1036	Sequence 1036, Ap
185.4	6.9	3921	18	US-10-287-226-319	Sequence 319, App
185.4	6.9	3921	19	US-10-648-593-1	Sequence 1, Appli
185.4	6.9	3921	20	US-10-473-974-223	Sequence 223, App
185.4	6.9	3921	21	US-10-616-403-5	Sequence 5, Appli
185.4	6.9	3921	21	US-10-897-711-1	Sequence 1, Appli
176.2	6.6	1518	18	US-10-280-576-24	Sequence 24, Appl
174.6	6.5	1816	19	US-10-377-268-3	Sequence 3, Appli
174.6	6.5	1050	19	US-10-377-268-4	Sequence 4, Appli
174.6	6.5	3030	16	US-10-325-430-8	Sequence 8, Appli
174.6	6.5	3416	8	US-08-987-689A-1	Sequence 1, Appli
174.6	6.5	3416	15	US-10-292-524-1	Sequence 1, Appli
174.6	6.5	3416	17	US-10-464-805-2	Sequence 2, Appli
174.6	6.5	3416	17	US-10-305-720-1483	Sequence 1483, Ap
174.6	6.5	3416	21	US-10-860-066-1	Sequence 1, Appli
174.6	6.5	3544	14	US-10-161-803-51	Sequence 51, Appl
174.6	6.5	4089	17	US-10-291-808-13	Sequence 13, Appl
174.6	6.5	4089	19	US-10-620-052A-7	Sequence 7, Appli
174.6	6.5	4151	14	US-10-161-803-52	Sequence 52, Appl
174.6	6.5	4151	16	US-10-325-430-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-10-003-295-1
; Sequence 1, Application US/10003295
; Publication No: US20020168741A1
; GENERAL INFORMATION:
; APPLICANT: GAW, Weinliu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01183DIV
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-003-295-1

Query Match	100.0%;	Score 2674;	DB 13;	Length 2674;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2674;	Conservative	0;	Mismatches	0;
			Indels	0;
				Gaps
				0;
Qy	1	TCCGGGGTCCGACCGGGCTGAGTCGGTCCGAGGCGCTCCGAGGAGCAGCTCCCGTGC	60	
Db	1	TCCGGGGTCCGACCGGGCTGAGTCGGTCCGAGGCGCTCCGAGGAGCAGCTCCCGTGC	60	
Qy	61	GGAAACAGCACTATGGGCTTCTCTTGTGAGTGTGAGCCCCCAGGCGGTCCTGTC	120	

Db	61	GGAAACAGCACTATGGGCTCTTCTTCTAGAGTGTGCAGCCCCCAGGGGCCACGGGGTCTCTGC	120
Qy	121	AGCAATGCAGGAGGCCGAGCTTCGTCTACTGAGGGCAATGAGAAAGTGGATGCCCCAGC	180
Db	121	AGCAATGCAGGAGGCCGAGCTTCGTCTACTGAGGGCAATGAGAAAGTGGATGCCCCAGC	180
Qy	181	GGGTCAAGAGTGA CAGGAGATATGCGAGACTGCTTACACATGTCTCCCTGCAGACAGTG	240
Db	181	GGGTCAAGAGTGA CAGGAGATATGCGAGACTGCTTACACATGTCTCCCTGCAGACAGTG	240
Qy	241	GGGGCCAGAGCCCGGGCCATCAGCCCTGACAGGCCCATCAGTCAGTCCTTGGGCTCAGATCA	300
Db	241	GGGGCCAGAGCCCGGGCCATCAGCCCTGACAGGCCCATCAGTCAGTCCTTGGGCTCAGATCA	300
Qy	301	CCAGCCAAACTGAGGGCCTGAGCGCTTCTCGGGCAGCA GCAGAGGATCTGAACCTCAG	360
Db	301	CCAGCCAAACTGAGGGCCTGAGCGCTTCTCGGGCAGCA GCAGAGGATCTGAACCTCAG	360
Qy	361	GGCCCTTGAGCAGCTGAGCTGCTCATCCGGGACGGCAGCAGCTTCGCAAGACCTTACA	420
Db	361	GGCCCTTGAGCAGCTGAGCTGCTCATCCGGGACGGCAGCAGCTTCGCAAGACCTTACA	420
Qy	421	CGCAGCAGTGGCAGCAGCTCAGCAGAGGCTCACMAAGACCACAGCCAGGACATTTGAGA	480
Db	421	CGCAGCAGTGGCAGCAGCTCAGCAGAGGCTCACMAAGACCACAGCCAGGACATTTGAGA	480
Qy	481	AGCTGAGAGCCAGTACCGAGCTTGCGACCGGACAGTGCCTCCAAAGCGCAAGCGCAAGTACC	540
Db	481	AGCTGAGAGCCAGTACCGAGCTTGCGACCGGACAGTGCCTCCAAAGCGCAAGCGCAAGTACC	540
Qy	541	AGGAGGCCAGCAAAAGACAAAGACCGTGACAAAGCCAAAGACAAGATGTGCGCAGCCTGT	600
Db	541	AGGAGGCCAGCAAAAGACAAAGACCGTGACAAAGCCAAAGACAAGATGTGCGCAGCCTGT	600
Qy	601	GGAGCTCTTTGCTCACCAACCGCTATGTCTGGCGCTGCGGGCTGCGCAGCTACACC	660
Db	601	GGAGCTCTTTGCTCACCAACCGCTATGTCTGGCGCTGCGGGCTGCGCAGCTACACC	660
Qy	661	ACCAGCACCAACAGAGCTCTGTGTCGCGGCTGTGCGGTCACTGCAAGACCTTGACG	720
Db	661	ACCAGCACCAACAGAGCTCTGTGTCGCGGCTGTGCGGTCACTGCAAGACCTTGACG	720
Qy	721	AGGAGATGCTTGCACTCTGAAGAGAGATCTTGACAGGAATACCTGGAGATTTAGCAGCTGG	780
Db	721	AGGAGATGCTTGCACTCTGAAGAGAGATCTTGACAGGAATACCTGGAGATTTAGCAGCTGG	780
Qy	781	TGCAGGATGAGTGTGTGCCATTACCCGGGAGATGGCTGCAGCTGTGCCCGCATCCAGC	840
Db	781	TGCAGGATGAGTGTGTGCCATTACCCGGGAGATGGCTGCAGCTGTGCCCGCATCCAGC	840
Qy	841	CTGAGGCTGAGTACCAAGGCTTCTGCGACAGTATGGGTCCGACCTTGACGCTCCACCT	900
Db	841	CTGAGGCTGAGTACCAAGGCTTCTGCGACAGTATGGGTCCGACCTTGACGCTCCACCT	900
Qy	901	GTGTCAAGTTCGATGAGTCACTGTGTGAGGAGGTGAACCGCTGGAGCCTTGGGGAGCTCC	960
Db	901	GTGTCAAGTTCGATGAGTCACTGTGTGAGGAGGTGAACCGCTGGAGCCTTGGGGAGCTCC	960
Qy	961	AGCTGAACAGCTGACTGTGGAGCGGTGCAGCA CAGCTGACCTCAGTGACAGATGAGC	1020
Db	961	AGCTGAACAGCTGACTGTGGAGCGGTGCAGCA CAGCTGACCTCAGTGACAGATGAGC	1020
Qy	1021	TGGCTGTGGCCACCGAGATGGTGTTCAGCGGCGAGGAGATGGTTACCGAGCTGCACAGG	1080
Db	1021	TGGCTGTGGCCACCGAGATGGTGTTCAGCGGCGAGGAGATGGTTACCGAGCTGCACAGG	1080
Qy	1081	AGCTCGGAATGAAGAGGAGAACCCACCCCGGAGCGGTGCAGCTGCTGGGCAAGA	1140
Db	1081	AGCTCGGAATGAAGAGGAGAACCCACCCCGGAGCGGTGCAGCTGCTGGGCAAGA	1140
Qy	1141	GGCAAGTGTCTGCAAGAGCACTGCAGGGGCTGCAGGTAGCGCTGTGCAGCCAGGCCAAGC	1200
Db	1141	GGCAAGTGTCTGCAAGAGCACTGCAGGGGCTGCAGGTAGCGCTGTGCAGCCAGGCCAAGC	1200

QY	1201	TGCAGGCCCAGCAGGAGTTGCTGCAGAGCAAAAGCTGGAGCACCTGGGCCCGCGGAGCCCC	1260
DB	1201	TGCAGGCCCAGCAGGAGTTGCTGCAGAGCAAAAGCTGGAGCACCTGGGCCCGCGGAGCCCC	1260
QY	1261	CGCTGTGCTGCTCTCTGCAGGATGACCGCCACTCACGTCGTCTCTCGGAGCAGAGCGAG	1320
DB	1261	CGCTGTGCTGCTCTCTGCAGGATGACCGCCACTCCTCACGTCGTCTCTCGGAGCAGAGCGAG	1320
QY	1321	AGGGGGAAGGACACCCAGCTGGAGATCCTTAAAGGCCACATCTCAGGAATCTTCGGCC	1380
DB	1321	AGGGGGAAGGACACCCAGCTGGAGATCCTTAAAGGCCACATCTCAGGAATCTTCGGCC	1380
QY	1381	CCAAAGTTCTCGAAACCTGTATCCGACTGGAAGGGAAAGGCTTTCCTAGCATTTCTTGTCTCA	1440
DB	1381	CCAAAGTTCTCGAAACCTGTATCCGACTGGAAGGGAAAGGCTTTCCTAGCATTTCTTGTCTCA	1440
QY	1441	TCGACCACTTACTGAGCACCACGAGCCCTCACCAGAGAGTGGTGTGTCTCTGCACA	1500
DB	1441	TCGACCACTTACTGAGCACCACGAGCCCTCACCAGAGAGTGGTGTGTCTCTGCACA	1500
QY	1501	GGGCTGTGCCCAAGGACAAGTGGGTCTGAAACAATGAGACCTGGTGTGGTGGAGCAGA	1560
DB	1501	GGGCTGTGCCCAAGGACAAGTGGGTCTGAAACAATGAGACCTGGTGTGGTGGAGCAGA	1560
QY	1561	TTGAGCGGGGAACTTTTGGCGAAGTGTTCAGCGGACGCTCGGAGCCGACCAACACCCCTGG	1620
DB	1561	TTGAGCGGGGAACTTTTGGCGAAGTGTTCAGCGGAGCGCTCGGAGCGCTCGGAGCGACACCCCTGG	1620
QY	1621	TGGCGGTGAACTGTTGTTCGAGAGACGCTCCACCTGACCTCAAGGCCAAGTTTCTACAGG	1680
DB	1621	TGGCGGTGAACTGTTGTTCGAGAGACGCTCCACCTGACCTCAAGGCCAAGTTTCTACAGG	1680
QY	1681	AAGCAGAGATCCTGACGAGTACAGCACCCCAACATCGTGGGTCTCATTTGGTGTCTGCA	1740
DB	1681	AAGCAGAGATCCTGACGAGTACAGCACCCCAACATCGTGGGTCTCATTTGGTGTCTGCA	1740
QY	1741	CCCAGAACGAGCCCATCTACATCGTCTATGGAGCTTTGCAAGGGGGGCGACTTCTCTGACCT	1800
DB	1741	CCCAGAACGAGCCCATCTACATCGTCTATGGAGCTTTGCAAGGGGGGCGACTTCTCTGACCT	1800
QY	1801	TCCTCCGACGAGGGGGCCCGCTCGGGGTGAAGACTCTGCTGCAGAGATGGTGGGGGATG	1860
DB	1801	TCCTCCGACGAGGGGGCCCGCTCGGGGTGAAGACTCTGCTGCAGAGATGGTGGGGGATG	1860
QY	1861	CAGCTGTGGCATGAGTAACTTGGAGAGCAAGTGTCTGCATCCAACGGGACCTTGGCTGTCTC	1920
DB	1861	CAGCTGTGGCATGAGTAACTTGGAGAGCAAGTGTCTGCATCCAACGGGACCTTGGCTGTCTC	1920
QY	1921	GGAACTGCTGTGTGACAGAGAGAAATGCTCTGAAGATCAGTGAATTTGGGATGTCCTCGAG	1980
DB	1921	GGAACTGCTGTGTGACAGAGAGAAATGCTCTGAAGATCAGTGAATTTGGGATGTCCTCGAG	1980
QY	1981	AGGAAGCCCATGGGGTCTATGCAAGCTCAGGGGGCCCTCAGACAAAGTCCCCGTGAAAGTGA	2040
DB	1981	AGGAAGCCCATGGGGTCTATGCAAGCTCAGGGGGCCCTCAGACAAAGTCCCCGTGAAAGTGA	2040
QY	2041	CCGCACCTGAGGCCCTTAACTACGCCGCGTACTCTCCGAAGCGACGTGTGGAGGCTTTC	2100
DB	2041	CCGCACCTGAGGCCCTTAACTACGCCGCGTACTCTCCGAAGCGACGTGTGGAGGCTTTC	2100
QY	2101	GCATCTTGCTCTGGGAGACTTTCAGCCTTGGGGCCCTCCCCCTATATCCCAAACCTCAGCAATC	2160
DB	2101	GCATCTTGCTCTGGGAGACTTTCAGCCTTGGGGCCCTCCCCCTATATCCCAAACCTCAGCAATC	2160
QY	2161	AGCAGACACGGGAGTTTGTGGAGAAAGGGGGCCGTCTGCCCTGCCAGAGCTGTGTCTCTG	2220
DB	2161	AGCAGACACGGGAGTTTGTGGAGAAAGGGGGCCGTCTGCCCTGCCAGAGCTGTGTCTCTG	2220
QY	2221	ATGCCGTGTTTCAGGCTCATGGAGCTGTGGGCTATGAGCCTTGGGAGCGGCGCCAGCT	2280
DB	2221	ATGCCGTGTTTCAGGCTCATGGAGCTGTGGGCTATGAGCCTTGGGAGCGGCGCCAGCT	2280

Db 2638 TCCGAAAGCGGCATCGTGAGGCTGGAGCCGCCCTTCTCAAGCTGGTGGCTCTGACGGCC 2697
QY 2371 TAGGTGAGCTCTCAGCGCTCCAGCTCATATGCTGACAGCTCTTCACAGTCTCTGGACT 2430
Db 2698 TAGGTGAGCTCTCAGCGCTCCAGCTCATATGCTGACAGCTCTTCACAGTCTCTGGACT 2757
QY 2431 CTTGCCACAGCATCCACACTGCGGACAGATGACGCGGCTGCTCTCTGTGTCCCTG 2490
Db 2758 CTTGCCACAGCATCCACACTGCGGACAGATGACGCGGCTGCTCTCTGTGTCCCTG 2817
QY 2491 CTTGCTGACAGGCTCTCTCTCCGGCAGAAACAATAAAACCACTTTGTGCCCACTGAAA 2550
Db 2818 CTTGCTGACAGGCTCTCTCTCTCCGGCAGAAACAATAAAACCACTTTGTGCCCACTGAAA 2877
QY 2551 AAAAAAAAAA 2560
Db 2878 AAAAAAAAAA 2887

RESULT 4

US-10-003-295-3
; Sequence 3, Application US/10003295
; Publication No. US20020168741A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weinu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIV
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15297
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-003-295-3

Query Match 13.6%; Score 362.4; DB 13; Length 15297;
Best Local Similarity 99.7%; Pred. No. 1.3e-46;
Matches 363; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2187 GGGGGCGCTGTCCCTGCCAGAGCTGTGCTCCTGATGCCGCTGTTCAGGCTCATGGAGCAG 2246
Db 12938 GGGGGCGCTGTCCCTGCCAGAGCTGTGCTCCTGATGCCGCTGTTCAGGCTCATGGAGCAG 12997
QY 2247 TGCTGGGCTATGAGCTGGGACGCGCCAGCTTACAGACCATCTACAGAGAGCTGCAG 2306
Db 12998 TGCTGGGCTATGAGCTGGGACGCGCCAGCTTACAGACCATCTACAGAGAGCTGCAG 13057
QY 2307 AGCATCCGAAAGCGGCATCGTGAGGCTGGGACCCCTTCTCAAGCTGGTGGCTCTGCA 2366
Db 13058 AGCATCCGAAAGCGGCATCGTGAGGCTGGGACCCCTTCTCAAGCTGGTGGCTCTGCA 13117
QY 2367 GGCCTAGGTGAGCTCTCCTCAGCGGCTCAGCTCATATGCTGACAGCTCTTCACAGTCTTG 2426
Db 13118 GGCCTAGGTGAGCTCTCCTCAGCGGCTCAGCTCATATGCTGACAGCTCTTCACAGTCTTG 13177
QY 2427 GACTCTGCTGACAGCTATGAGCTGGGACGCGCCAGCTTACAGACCATCTACAGAGAGCTGCAG 2486
Db 13178 GACTCTGCTGACAGCTATGAGCTGGGACGCGCCAGCTTACAGACCATCTACAGAGAGCTGCAG 13237
QY 2487 CTTGCTGCTGACAGGCTCTCTCTCCGGGAGAAACAATAAAACCACTTTGTGCCCACTG 2546
Db 13238 CTTGCTGCTGACAGGCTCTCTCTCTCCGGGAGAAACAATAAAACCACTTTGTGCCCACTG 13297
QY 2547 AAAA 2550
Db 13298 AACA 13301

RESULT 5

US-10-660-763-3
; Sequence 3, Application US/10660763
; Publication No. US20040063130A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weinu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIV
; CURRENT APPLICATION NUMBER: US/10/660,763
; CURRENT FILING DATE: 2003-09-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15297
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-660-763-3

Query Match 13.6%; Score 362.4; DB 18; Length 15297;
Best Local Similarity 99.7%; Pred. No. 1.3e-46;
Matches 363; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2187 GGGGGCGCTGTCCCTGCCAGAGCTGTGCTCCTGATGCCGCTGTTCAGGCTCATGGAGCAG 2246
Db 12938 GGGGGCGCTGTCCCTGCCAGAGCTGTGCTCCTGATGCCGCTGTTCAGGCTCATGGAGCAG 12997
QY 2247 TGCTGGGCTATGAGCTGGGACGCGCCAGCTTACAGACCATCTACAGAGAGCTGCAG 2306
Db 12998 TGCTGGGCTATGAGCTGGGACGCGCCAGCTTACAGACCATCTACAGAGAGCTGCAG 13057
QY 2307 AGCATCCGAAAGCGGCATCGTGAGGCTGGGACCCCTTCTCAAGCTGGTGGCTCTGCA 2366
Db 13058 AGCATCCGAAAGCGGCATCGTGAGGCTGGGACCCCTTCTCAAGCTGGTGGCTCTGCA 13117
QY 2367 GGCCTAGGTGAGCTCTCCTCAGCGGCTCAGCTCATATGCTGACAGCTCTTCACAGTCTTG 2426
Db 13118 GGCCTAGGTGAGCTCTCCTCAGCGGCTCAGCTCATATGCTGACAGCTCTTCACAGTCTTG 13177
QY 2427 GACTCTGCTGACAGCTATGAGCTGGGACGCGCCAGCTTACAGACCATCTACAGAGAGCTGCAG 2486
Db 13178 GACTCTGCTGACAGCTATGAGCTGGGACGCGCCAGCTTACAGACCATCTACAGAGAGCTGCAG 13237
QY 2487 CTTGCTGCTGACAGGCTCTCTCTCCGGGAGAAACAATAAAACCACTTTGTGCCCACTG 2546
Db 13238 CTTGCTGCTGACAGGCTCTCTCTCTCCGGGAGAAACAATAAAACCACTTTGTGCCCACTG 13297
QY 2547 AAAA 2550
Db 13298 AACA 13301

RESULT 6

US-10-887-553A-240
; Sequence 240, Application US/10887553A
; Publication No. US20050085436A1
; GENERAL INFORMATION:
; APPLICANT: Garza, Dan
; APPLICANT: Li, Hao
; TITLE OF INVENTION: Method to treat conditions associated
; TITLE OF INVENTION: with insulin signalling dysregulation
; FILE REFERENCE: 4-33262
; CURRENT APPLICATION NUMBER: US/10/887,553A
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: 60/485,883
; PRIOR FILING DATE: 2003-08-07
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 240
; LENGTH: 2950
; TYPE: DNA
; ORGANISM: human
US-10-887-553A-240

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Query Match      12.3%; Score 328.8; DB 21; Length 2950;
Best Local Similarity 62.0%; Pred. No. 1.5e-41;
Matches 573; Conservative 0; Mismatches 342; Indels 9; Gaps 3;

Qy 1392 AACCTGTACCACTGGAAGGGAAGGCTTCTCTAGCATTCTTTGCTCATCGACCACTTA 1451
Db 1918 AACATGTATCGAATTCGAGGGCACTGGGTTTTCAACACATTCCTCAACTTATAGATCATCAC 1977
Qy 1452 CTGAGCACCAGCAGCCCTCACCAGAAGAGTGGTGTGCTGCACAGGCTGTGCCC 1511
Db 1978 TATACACAAACACAGGTATCATCACTAAGAAATCAGGTGTAGTTCCTGTAATCTTATCTCT 2037
Qy 1512 AAGGACAAG---TGGTGTCTGAAACATGAGACCTGTGTTGGTGTGACAGATTGGACGG 1568
Db 2038 AAGGACAAGAAATGGATTCTCAGTCATCAAGATGTATATTGGGAGAATTACTGGCAAG 2097
Qy 1569 GGGAACTTTGGGAAGTGTTCAGCGGAGCGCTCGGCGCCGACACACACCTGTGCGCGTG 1628
Db 2098 GGAATTTTGGTGAAGTATATAGG---GCACATTAAGGATTAACAACTTCTGTGCTGTT 2154
Qy 1629 AAGTCTTGTGAGAGACGCTCCACACCTCAAGCCCAAGTTTCTACAGGAAGCGAGG 1688
Db 2155 AAAACATGTAAGAGATCTTCTCAGGAATTGAAATTAATAATTTTACAGAAGCCCAA 2214
Qy 1689 ATCTGAAGCAGTACAGCCACCCCAACATCGTGGCTCTCATTTGGTGTCTGCACCAGAAG 1748
Db 2215 ATTCTCAAGCAATATGATCATCCCAATATTGTCAAACTTATAGGAGTTTGCACACAAGA 2274
Qy 1749 CAGCCCATCTACATCGTATGAGACCTTGTGAGGGGGGCGACTTCTGACCTTCTCCGC 1808
Db 2275 CAGCCTGTCTACATCATTTAGGAAGTGTGTTTCAGGAGGTGATTTCTCACCTTTCTGAGA 2334
Qy 1809 ACGGAGGGGGCCCTCGCGGTCAAGACTCTGCTGACAGATGTTGGGGATGACAGCTGCT 1868
Db 2335 AGGAAGAGGATGAACCTAAACTCAACAGTTAGTGAATTTTCATTAGACGCTGCTGCT 2394
Qy 1869 GGATGAGTACCTTGGAGAGCAAGTGTCTGCAATCCACCGGACCTGGCTGCTCGGAAGTGC 1928
Db 2395 GGTATGTTGATCTCGAGAGTAAATACTGTATACACAGGAGACCTTGTGCAAGAAACTGC 2454
Qy 1929 CTGCTGACAGAGAATGCTCAAGATCAGTGAACATTTGGGATGTCGAGAGGAAGACC 1988
Db 2455 CTGCTAGGTGAAAATAATGTTCTGAAAATCAGTGAATTTGGAATGTCTCGTCAAGAGGAT 2514
Qy 1989 GATGGGTCTATGAGCTCAGGGGGCTCAGACAACTCCCGTGAAGTGGACCGCACCT 2048
Db 2515 GGTGGAGTATTCATCTTC---TGGCTTAAGCAGATTTCCATTAATGACAGACCG 2571
Qy 2049 GAGCCCTTAACTACGGCGCTACTCTCTCGAAAGCGACGTGTGGAGCTTTGGCATCTTG 2108
Db 2572 GAAGCTCTTAATTATGGAGATACAGTTACAGAGATGACGTGTGGAGCTTTGGCATCCTT 2631
Qy 2109 CTCTGGAGACCTTCAGCTGGGGGCTCCCGCTATCCAACTCAGGAATCAGACACA 2168
Db 2632 CTCTGGAGACCTTCAGCTTAGGGGTTTGTCCGTACCTCGAATGACAAATCAGCAAGCA 2691
Qy 2169 CGGAGTTTGGGAGAAGGGGGCGCTGCTGCGCTCCCGACAGAGTGTCTGTATGCGGTG 2228
Db 2692 AGAGACAGTAGAAGAGGATACCGGATGTACCTCCCGACACTGTCCAGAGGATATT 2751
Qy 2229 TTCAGGCTCATGAGCAGTGTCTGGGCTTATGAGCTGTGGGCGGCGCCAGCTTCAGCAC 2288
Db 2752 TCCAAATCATGATGAGTGTGGGATTAATAACCTGAAATCGCCCTAAGTTTCAGTGAA 2811
Qy 2289 ATCTACAGGAGCTGCAGAGATC 2312
Db 2812 CTTCAGAAAGAGCTCACTATCATC 2835
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RESULT 7
US-09-918-995-1503
; Sequence 1503, Application US/09918995

Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1503
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(449)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-1503

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Query Match      12.2%; Score 326.8; DB 10; Length 449;
Best Local Similarity 99.4%; Pred. No. 2.4e-41;
Matches 328; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1778 GCAGGGGGGGGACTTCTCTGACCTTCTCCGACGAGGGGGGGCGCTGCGGGTGAAGAC 1837
Db 120 GCAGGGGGGGGACTTCTGACCTTCTCCGACGAGGGGGGGCGCTGCGGGTGAAGAC 179
Qy 1838 TCTGTGTCAGATGGTGGGGATGCAGCTGTGTCATGGAGTACCTGAGACAAAGTGTG 1897
Db 180 TCTGTGTCAGATGGTGGGGATGCAGCTGTGTCATGGAGTACCTGAGACAAAGTGTG 239
Qy 1898 CATCCACCGGAGCTGGCTCTCGGAACCTGCTGTCGACAGAGAGAAATGTCTGGAAGAT 1957
Db 240 CATCCACCGGAGCTGGCTCTCGGAACCTGCTGTCGACAGAGAGAAATGTCTGGAAGAT 299
Qy 1958 CAGTGACTTTGGGATGTCCCGAGAGGAAGCGGATGCGGTCTATGCAGCTCAGGGGGCCT 2017
Db 300 CAGTGACTTTGGGATGTCCCGAGAGGAAGCGGATGCGGTCTATGCAGCTCAGGGGGCCT 359
Qy 2018 CAGCAAGTCCCGTGAAGTGGACCGACCTGAGGGCCCTTAACTACGGCGCTACTCCTC 2077
Db 360 CAGCAAGTCCCGTGAAGTGGACCGACCTGAGGGCCCTTAACTACGGCGCTACTCCTC 419
Qy 2078 CGAAGGAGCTGTGGAGCTTTGGCATCTT 2107
Db 420 CGAAGGAGCTGTGGAGCTTTGGCATCTT 449
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RESULT 8
US-09-948-802-5
; Sequence 5, Application US/09948802
; Publication No. US20020172981A1
; GENERAL INFORMATION:
; APPLICANT: ROBISON, KEITH E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
; FILE REFERENCE: WNI-090
; CURRENT APPLICATION NUMBER: US/09/948,802
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 09/387,212
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 361
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: All occurrences of n indicate any nucleotide
US-09-948-802-5

Query Match 11.1%; Score 296.2; DB 9; Length 361;
Best Local Similarity 97.4%; Pred. No. 1.2e-36;
Matches 333; Conservative 0; Mismatches 4; Indels 5; Gaps 3;
QY 1684 CGAGGATCTGAAGCAGTACAGCCACCCCAACATCGTGGTCTCATTTGGTGTCTGCACCC 1743
DB 20 CNAAGGATCTGAAGCAGTACAGCCACCCCAACATCGTGGTCTCATTTGGTGTCTGCACCC 79
QY 1744 AGAAGCAGCCCATCTACATCGTTCATGGAGCTTGTGCAGGGGGCGGACTTCTTGACCTTCC 1803
DB 80 AGAAGCAGCCCATCTACATCGTTCATGGAGCTTGTGCAGGGGGCGGACTTCTTGACCTTCC 139
QY 1804 TCCGACGAGGGGGCCCGCTGGGTGAAGACTCTGTGCAGATGTGGGGATGCAG 1863
DB 140 TCCGACGAGGGGGCCCGCTGGGTGAAGACTCTGTGCAGATGTGGGGATGCAG 199
QY 1864 CTGCTGGCATGGATCTCGAGAGCAAGTGTCTGATCCACCGGACCTGGTGTCTCGGA 1923
DB 200 CTGCTGGCATGGATCTCGAGAGCAAGTGTCTGATCCACCGGACCTGGTGTCTCGGA 259
QY 1924 ACTGCTGGTGCACAGAGAAGATCTCTGAAG-ATCAGTGACTTT-GGGATGTCCCGAGA 1981
DB 260 ACTGCTGGTGCACAGAGAAGATCTCTGGAAGATCAGTGACTTTGGGGATGTCCCGAGA 319
QY 1982 GGAAGCC---GATGGGTCTATGCAGCCTCAGGGGGCCTCAG 2020
DB 320 GGAAGCCCGATTGGGGTCTATGCAGCCTCAGGGGGCCTCAG 361

RESULT 9

US-10-121-925-5
; Sequence 5, Application US/10121925
; Publication No. US20030104505A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, KEITH E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; FILE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR
; FILE REFERENCE: MNI-090
; CURRENT APPLICATION NUMBER: US/10/121,925
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: US/09/948,802
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 09/387,212
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 361
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: All occurrences of n indicate any nucleotide
US-10-121-925-5

Query Match 11.1%; Score 296.2; DB 15; Length 361;
Best Local Similarity 97.4%; Pred. No. 1.2e-36;
Matches 333; Conservative 0; Mismatches 4; Indels 5; Gaps 3;
QY 1684 CGAGGATCTGAAGCAGTACAGCCACCCCAACATCGTGGTCTCATTTGGTGTCTGCACCC 1743
DB 20 CNAAGGATCTGAAGCAGTACAGCCACCCCAACATCGTGGTCTCATTTGGTGTCTGCACCC 79
QY 1744 AGAAGCAGCCCATCTACATCGTTCATGGAGCTTGTGCAGGGGGCGGACTTCTTGACCTTCC 1803
DB 80 AGAAGCAGCCCATCTACATCGTTCATGGAGCTTGTGCAGGGGGCGGACTTCTTGACCTTCC 139
QY 1804 TCCGACGAGGGGGCCCGCTGGGTGAAGACTCTGTGCAGATGTGGGGATGCAG 1863
DB 140 TCCGACGAGGGGGCCCGCTGGGTGAAGACTCTGTGCAGATGTGGGGATGCAG 199
QY 1864 CTGCTGGCATGGATCTCGAGAGCAAGTGTGATCCACCGGACCTGGTGTCTCGGA 1923

DB 200 CTGCTGGCATGGAGTACCTGGAGAGCAAGTGTCTCATCCACCGGACCTGGTGTCTCGGA 259
QY 1924 ACTGCTGGTGCACAGAGAAGATGTCTCTGAAG-ATCAGTGACTTT-GGGATGTCCCGAGA 1981
DB 260 ACTGCTGGTGCACAGAGAAGATGTCTCTGAAGATCAGTGACTTTGGGGATGTCCCGAGA 319
QY 1982 GGAAGCC---GATGGGTCTATGCAGCCTCAGGGGGCCTCAG 2020
DB 320 GGAAGCCCGATTGGGGTCTATGCAGCCTCAGGGGGCCTCAG 361
RESULT 10
US-10-280-576-19
; Sequence 19, Application US/10280576
; Publication No. US20040044405A1
; GENERAL INFORMATION:
; APPLICANT: Wolfe, Matthew R.
; TITLE OF INVENTION: VASCULAR STENT OR GRAFT COATED OR IMPREGNATED WITH PROTEIN
; FILE REFERENCE: 09820.189
; CURRENT APPLICATION NUMBER: US/10/280,576
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 60/343,732
; PRIOR FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 19
; LENGTH: 1779
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-10-280-576-19

Query Match 10.2%; Score 271.6; DB 18; Length 1779;
Best Local Similarity 57.0%; Pred. No. 9.3e-33;
Matches 518; Conservative 0; Mismatches 384; Indels 6; Gaps 1;
QY 1398 TACCGACTCGAAGGGGAGGCTTCTCAGCATCTCTTCTCATCGACCCTACTCTGAGC 1457
DB 844 TTCCGGTTCGAGGGACCACCATTTGCCAGCATCCAGGAGCTGATCATGATCAGTATCAC 903
QY 1458 ACCCAGCAGCCCTCCACCAAGAGAGTGTGTGTCTCTGCACAGGCTGTGCCAAGGAC 1517
DB 904 TCGGAATTCGAGTGACCGTGAAATCGGGAGCCATCTCCGACGACCCGTTTGCCTGGAG 963
QY 1518 AAGTGGTGTGAACCATGAGGACCTGGTGTGGGTGAGCAGATTTGGAGGGGGAATTT 1577
DB 964 CGCTGGGAGCTGAGCAACGATGATGTGTCTCTGAGGAGGATTTGTCGGGGAATTTT 1023
QY 1578 GCGGAAGTGTTCAGCGGACCGCTCGAGCGCAACACACCTGTGGTGGGTGAACTTTGT 1637
DB 1024 GGGGATGTCTAAGGCCAACTGAAGTCCACCAACTGGATGTGGCTGTCAAAACCTGT 1083
QY 1638 CGAGAGACGCTCCACCTGACCTCAAGGCCAAGTTTCTCAGGAAGCGAGGATCTCTGAAG 1697
DB 1084 CGAATGACCTTCGCCCGACGAAAGAGCGTAAATTCCTACAGGAAGGGCGCATCTCAAG 1143
QY 1698 CAGTACAGCCACCCCAACATCGTCTCATTTGGTGTCTGCACCAGAGAGCCCATC 1757
DB 1144 CAATACGATCATCAAAATATCGTAAATTTGATTTGGCATTTGTGTGAGAAGAGGCCATC 1203
QY 1758 TACATCGTTCATGGAGCTTGTGCAGGGGGGCGGACTTCTGACCTTCTCTCCAGCGGGG 1817
DB 1204 ATGATTTGATGAAATTTGGTGTCTCGTGGTGTCTTAACTTTTACGCAAGAACTCC 1263
QY 1818 GCCCGCTCGGGGTGAAGACTCTGTGCAGATGTGGGGGATGCAGCTGTGCATCGAG 1877
DB 1264 AATGGCTCCACCTCCCAACAAATGGGATGTGCAGAGATCGCGGGCAGGATCCGA 1323
QY 1878 TACCTGAGAGCAAGTCTGCATCCACCGGGAAGCTGGTGTCTCTCGGAATCTGCTGGTGA 1937
DB 1324 TATCTGAGTCCAAAACATTCATTCGCGATCTGCGGGGGTAAATTTGCTCTGTTGAC 1383
QY 1938 GAGAAGAAATGTCTGAAAGATCAGTGAATTTGGGATGTCCCGAGAGGAGCGGATGGGTC 1997

Db 1384 TTGGAGCAGTGTGAAGATCTCCGATTCGGAATGTCCTCGGAGAA-----GAGAA 1437
Qy 1998 TATGAGCCTCAGGGGGCTCAGCAAGTCCCCTGTAAGTGGACCGCACCTTGAGGCCCTT 2057
Db 1438 TATATAGTTTCCGATGGCATGAAACAAATACCTGTGAAGTGGACAGCTCCCGAGCCCTG 1497
Qy 2058 AACTACGGCCCTACTCTCCGAAAGCAGCTGTGGAGCTTTGGCATCTTCTCTGGAG 2117
Db 1498 AATTTCGGCAAGTACACTTCGTGTGCGATGTGGTCTTATGGCATACTGATGTGGAG 1557
Qy 2118 ACCTTCAGCCTGGGGCCCTCCCTCTATCCCAACCTCAGCAATCAGCAGACCGGAGTTT 2177
Db 1558 ATCTTCTCAAGGGCGACACACCTTACTCCGGCATGACCACTCAGAGCCAGAGAGCGC 1617
Qy 2178 GTGAGAAAGGGGGCGCTCTCCCTGCGCCAGAGCTGTGTCTGTATGCGGTGTTGAGGCTC 2237
Db 1618 ATCGATACGGGATATCGTATGCCAAAGCGGAGAGCAGCCCGAGGAGATGTACCGACTG 1677
Qy 2238 ATGAGCAGTCTGGGCTATAGCCTGGGCGAGCGGGCCAGCTTCAGCACCATCTACCAG 2297
Db 1678 ATGCTCCAGTCTGGGCGAGCGCGCAATCCCGACCGCATTTTCGATGAGATCTACAAT 1737
Qy 2298 GAGCTGCA 2305
Db 1738 GTGTGGA 1745

RESULT 11

US-10-101-510-525
; Sequence 525, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/101.510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 525
; LENGTH: 3875
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-525

Query Match 7.5%; Score 201.2; DB 15; Length 3875;

Best Local Similarity 54.9%; Pred. No. 7.2e-22;

Matches 423; Conservative 0; Mismatches 338; Indels 9; Gaps 1;

Qy 1522 GGGTGCTGAACCATGAGGACCTGTGTGGTGAGCAGATTGGACGGGGNACTTTGGCG 1581
Db 1969 GGGAGCTTGATCCAGCGTGTGTGTGGACACTGTCTAGAGAGAGGAGTTTGGGG 2028
Qy 1582 AAGTGTTCAGCGGACGCTCGCAGCC-----GACAAACCCCTGTCGCGTGAAGT 1632
Db 2029 AAGTGTATGATGAGGACCTTGAGGCTCCCGACCCAGGACTGCAAGACTGTGCCATTAGA 2088
Qy 1633 CTTGTCGAGAGACGCTCCCACTGACCTCAAGGCCAAGTTTCTACAGAAAGCGAGGATCC 1692
Db 2089 CTTTAAAGACACATCCCGAGGTGGCAGTGTGGAACTTCCTTCGAGAGGCAACTATCA 2148
Qy 1693 TGAAGCAGTACAGCCACCCACATCGTGTCTCATTTGTCGTCGACCCAGAGAGC 1752
Db 2149 TGGGCGAGTTTAGCCACCCCGCATATTCGATCTGGAAGGCGTGTCAAAAGCGAAGC 2208
Qy 1753 CCATCTACATCGTCATGAGCTTGTGACAGGGGGCGACTTCCTGACCTTCTCCGCGACGG 1812
Db 2209 CGATCATGATCATACAGAAATTTATGGAGATGAGCCCTGGATCCCTTCCTGAGGAGC 2268
Qy 1813 AGGGGGCCCCCTGCGGGTGAAGACTCTGTCTGAGATGTTGGGGGATGCAAGCTCTCGCA 1872

Db 2269 GGGAGGACCAAGCTGGTCCCTGGGCGAGCTAGTGGCCATGTGCGAGGCGCATAGCATCTGGCA 2328
Qy 1873 TGGAGTACCTTGGAGAGCAAGTGTGATCCACCGGACCTGGGTGCTCGGAACCTGCTGG 1932
Db 2329 TGAACCTACCTCAGTATCAATATATGTCCACCGGACCTGGCTGCCAGAAACATCTGG 2388
Qy 1933 TGACAGAGAAGATGTCTCGAAGATCAGTCACTTTGGGATGTCCCGAGAGAAAGCCGATG 1992
Db 2389 TGAATCAAAACCTGTGTGCAAGGTGTCTGACTTTGGCCTGACTCGCCTCTCGATGACT 2448
Qy 1993 GGGTCTATGAGCCTCAGGGGGCTCAGACAAGTCCCGTGAAGTGGACCGCAGCTCAGG 2052
Db 2449 TTGATGGCACAATACGAAACCCAGGGAGGAAAGATCCCTATCCGTGGACAGCCCTGAAG 2508
Qy 2053 CCCTTAACTACGGCCGCTACTCTCCGAAAGCAGCTGTGGAGCTTTGGCATCTTGCTCT 2112
Db 2509 CCATTGCCCATCGATCTTACCACAGCAGCAGATGTGTGGAGCTTTGGGATTTGATGT 2568
Qy 2113 GGGAGACCTTTCAGCCTGGGGGCTCCCTTATCCCAACCTCAGCAATCAGCAGACAGGG 2172
Db 2569 GGGAGGTGTCTGAGCTTTGGGGCAAGCCTTATGGGAGATGAGCAATCAGAGGTTATGA 2628
Qy 2173 AGTTTGGAGAAGGGGGCGCTGCTGCCCTGCCAGAGCTGTCTCTGATGCCGTGTTCA 2232
Db 2629 AGAGCATTTGAGGATGGGTACCGGTGCCCCCTCTCTGTGGACTGCCCTCTCTGTATG 2688
Qy 2233 GGCTCATGAGCAGTGTGGGCTTATGAGCTGGGAGCGGCCAGCTTC 2282
Db 2689 AGCTCATGAAGAACTGCTGGGCATATGACCGTCCGCCGCCACACTTC 2738

RESULT 12

US-10-384-339C-1
; Sequence 1, Application US/10384339C
; Publication No. US20040175703A1
; GENERAL INFORMATION:
; APPLICANT: Kreutzer, Roland
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GE
; FILE REFERENCE: 20200/2002
; CURRENT APPLICATION NUMBER: US/10/384,339C
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/EP02/00152
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: DE 10100586.5
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: DE 10155280.7
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: DE 10158411.3
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: DE 10160151.4
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2955
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; TITLE: Eph A1
; PATENT DOCUMENT NUMBER: NM00532
US-10-384-339C-1

Query Match 7.4%; Score 198; DB 19; Length 2955;

Best Local Similarity 54.7%; Pred. No. 2.2e-21;

Matches 421; Conservative 0; Mismatches 340; Indels 9; Gaps 1;

Qy 1522 GGGTGTCTGAACCATGAGGACCTGTGTGGTGAGCAGATTGGACGGGGAACTTTGGCG 1581
Db 1874 GGGAGCTTGATCCAGCGTGTGCTGATGTGGACACTGTCTAGAGAGGAGAGTTTGGGG 1933
Qy 1582 AAGTGTTCAGCGGACCGCTGCGAGCC-----GACAAACCCCTGTGGCGGTGAAGT 1632


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Db 1934 AAGTGTATCGAGGACCTCAGGCTCCCGACGAGGACTGCAAGACTGTGGCCATTAGA 1993
Qy 1633 CTTGTTCGAGAGCGCTCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGGATCC 1692
Db 1994 CCTTAAAGACACATCCCAAGGTGGCCAGTGGTGAACCTTCTTCGAGAGGCAACTATCA 2053
Qy 1693 TGAAGCGTACAGGACCCCAACATCGTGGCTCTCATTTGGTGTCTGCACCCAGAACAGC 1752
Db 2054 TGGGCCAGTTTAGCCACCCCGCATATTCTGCATCTGGAAGCGGTCTGCACAAAGCGAAGC 2113
Qy 1753 CCATCTACATCGTCATGAGCTTGTGCGAGGGGCGACTTCTCGACTTCTCCCGCACGG 1812
Db 2114 CGATCATGATCATACAGAAATTTATGGAAGATCGAGCCCTGGATGCTTCTCGAGGAGC 2173
Qy 1813 AGGGGCGCCCTCGGGTGAAGACTCTGCTGCAGATGGTGGGGGATGAGAGTCTGTGGCA 1872
Db 2174 GGGAGGACCAAGCTGGTCCCTGGGCGAGCTAGTGGCCATGCTGCGAGGCGATAGCATCTGGCA 2233
Qy 1873 TGGAGTACCTGGAGAGCAAGTGTGCATCCACGGGACCTGGCTGCTCGAACTGCCTGG 1932
Db 2234 TGAATCAACCTGTGCTGCAAGTGTCTGACTTTGGCCCTGACTCGCCTCTCGATGACT 2293
Qy 1933 TGACAGAGAAGATGTCTCAAGATCAGTCACTTTGGGATGTCTCCGAGAGGAAGCGGATG 1992
Db 2294 TGAATCAAACTGTGCTGCAAGTGTCTGACTTTGGCCCTGACTCGCCTCTCGATGACT 2353
Qy 1993 GGGTCTATGAGCCTCAGGGGGCTCAGACAAAGTCCCGGTGAAGTGGACCGCACTGAGG 2052
Db 2354 TTGATGGCACATACGAACCCAGGAGGAAAGATCCCTATCCGTTGGACAGCCCTGAAG 2413
Qy 2053 CCCTTAACCTAGCGCGCTACTCTCCGAAAGCGAGTGTGGAGCTTTGGCATCTTGTCTCT 2112
Db 2414 CCAITGGCCATCGGATCTTACACACAGCAGATGTTGGAGCTTTGGATTTGTATGT 2473
Qy 2113 GGGAGACTTTCAGCCTGGGGCTTCCCTTATCCAACTCAGCAATCAGACAGACGGG 2172
Db 2474 GGGAGGTGCTGAGCTTTGGGACAAAGCTTATGGGAGATGAGCAATCAGAGGTTATGA 2533
Qy 2173 AGTTTGTGGAAAGGGGGCGTCTGCTGCCCGCCAGAGCTGTGCTGTGATGCCGTGTCA 2232
Db 2534 AGAGCAITGAGGATGGGTACCGGTGCCCCCTCTGTGGACTGCCCTGCCCCCTCTGTATG 2593
Qy 2233 GGCTCATGAGCACTGTCTGGCCCTATGAGCTGGGCGAGCGCCAGCTTC 2282
Db 2594 AGCTCATGAAGAACTGCTGGGCATATGACCGTGGCCCGCCGACACACTTC 2643

RESULT 13
US-09-967-768A-144
; Sequence 144, Application US/09967768A
; Patent No. US20020150877A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer
; FILE OF INVENTION: Sets
; FILE REFERENCE: 689290-72
; CURRENT APPLICATION NUMBER: US/09/967,768A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/60/236,109
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,034
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,111
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 144
; LENGTH: 3370
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-967-768A-144
Query Match 7.4%; Score 198; DB 9; Length 3370;
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Best Local Similarity 54.7%; Pred. No. 2.2e-21;
Matches 421; Conservative 0; Mismatches 340; Indels 9; Gaps 1;
Qy 1522 GGGTGTGAACCATGAGACCTGTGTGGTGTGAGCAGATTGGACGGGGAACTTTGGCG 1581
Db 1967 GGGAGCTTGTATCCAGCGTGGCTGATGGTGGACATGTCTATAGGAGAGAGAGTTGGGG 2026
Qy 1582 AAGTGTTCAGGGAGCGCTTGGAGCC-----GACAAACACCTGTGTGGGGTGAAGT 1632
Db 2027 AAGTGTATCGAAGGGACCTTCAGGGCTCCCGAGCCAGGACTGCAAGACTGTGGGCCATTAGA 2086
Qy 1633 CTGTGTGAGAGACGCTCCCACTGACCTCAAGGCCCAAGTTTCTACAGGAAGCGAGATCC 1692
Db 2087 CTTTAAAGACACATCCCGAGGTGGCCAGTGGTGAACCTTCTTCCAGAGGCAACTATCA 2146
Qy 1693 TGAAGCAGTACAGCCACCCCAACATCGTGGCTCTCATTTGGTGTCTGCAACCCAGAACGACG 1752
Db 2147 TGGGCGAGTTTAGCCACCCGCAATATTCTGCATCTCGAAGGGCTGCTCAAAAGCGAAAGC 2206
Qy 1753 CCATCTACATCGTATGAGCTTGTGAGGGGGGAGCTTCTGACCTTCTCCCGCACGG 1812
Db 2207 CGATCATGATCATACAGAAATTTATGGAAGATGAGCCCTGGATGCTTCTCGAGGAGC 2266
Qy 1813 AGGGGCGCCCTCGGGGTGAAGACTCTCTGCAGATGGTGGGGATGAGCTGTGGCA 1872
Db 2267 GGGAGGACGAGCTGGTCCCTGGGCGAGTAGTGGCCATGCTGCAGGGCATAGCATCTGGCA 2326
Qy 1873 TGGAGTACCTGAGAGCAAGTGTGCATCCACGGGACCTGGCTGCTCGAACTCCCTGG 1932
Db 2327 TGAACCTACCTCTAGTAAATCACAATATATGTCACCGGGACCTGGCTGCCAGAAACATCTTGG 2386
Qy 1933 TGACAGAGAAGAAATGTCTGGAAGATCAGTGACTTTTGGGATGTCCCGAGAGGAAGCGGATG 1992
Db 2387 TGAATCAAACTGTGCTGCAAGGTGTCTGACTTTGGCCTGACTCGCCTCTCGGATGACT 2446
Qy 1993 GGGTCTATGACGCTCAGGGGGCTCAGACAAAGTCCCGGTGAAGTGGACCGCACCTGAGG 2052
Db 2447 TTGATGGCACATACGAACCCAGGAGGAAAGATCCCTATCCGTTGGACAGCCCTGAAG 2506
Qy 2053 CCCTTAACCTAGCGCGCTACTCTCCGAAAGCGAGTGTGGAGCTTTGGCATCTTGTCTCT 2112
Db 2507 CCAITGGCCATCGGATCTTACACAGCAGCGATGTTGGAGCTTTGGATTTGTATGT 2566
Qy 2113 GGGAGACTTTCAGCCTGGGGCTTCCCTTATCCAACTCAGCAATCAGACAGACAGCGG 2172
Db 2567 GGGAGGTGCTGAGCTTTGGGGAACAGCCCTTATGGGAGATGAGCAATCAGGAGTTATGA 2626
Qy 2173 AGTTTGTGAGAGGGGGCGCTGCTGCCCTGCCAGAGCTGTGCTGATGCCGTGTCA 2232
Db 2627 AGAGCAITGAGGATGGGTACCGGTGCCCCCTCTGTGGACTGCCCTGCCCTCTGTATG 2686
Qy 2233 GGCTCATGAGCAGTGTCTGGGCTATGAGCTGGGCGAGCGCCAGCTTC 2282
Db 2687 AGCTCATGAAGAACTGCTGGGCATATGACCGTGGCCCGCCGACACACTTC 2736

RESULT 14
US-10-354-358-101
; Sequence 101, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Teal, Fong-Ying
; APPLICANT: Lesoon, Andrea
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Williamson, Mark
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
; TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
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;; TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
;; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
;; TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
;; TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
;; FILE REFERENCE: MPI02-020P1RNNMIM
;; CURRENT APPLICATION NUMBER: US/10/354.358
;; CURRENT FILING DATE: 2003-01-30
;; PRIOR APPLICATION NUMBER: US 60/353,600
;; PRIOR FILING DATE: 2002-01-31
;; PRIOR APPLICATION NUMBER: US 60/364,517
;; PRIOR FILING DATE: 2002-03-15
;; PRIOR APPLICATION NUMBER: US 60/371,075
;; PRIOR FILING DATE: 2002-04-09
;; PRIOR APPLICATION NUMBER: US 60/371,507
;; PRIOR FILING DATE: 2002-04-10
;; PRIOR APPLICATION NUMBER: US 60/372,984
;; PRIOR FILING DATE: 2002-04-16
;; PRIOR APPLICATION NUMBER: US 60/374,194
;; PRIOR FILING DATE: 2002-04-19
;; PRIOR APPLICATION NUMBER: US 60/382,995
;; PRIOR FILING DATE: 2002-05-24
;; PRIOR APPLICATION NUMBER: US 60/385,023
;; PRIOR FILING DATE: 2002-05-31
;; PRIOR APPLICATION NUMBER: US 60/388,853
;; PRIOR FILING DATE: 2002-06-14
;; PRIOR APPLICATION NUMBER: US 60/389,395
;; PRIOR FILING DATE: 2002-06-17
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 122
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 101
;; LENGTH: 3370
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (94)...(3048)
US-10-354-358-101

Query Match 7.4%; Score 198; DB 16; Length 3370;
Best Local Similarity 54.7%; Pred. No. 2.2e-21;
Matches 421; Conservative 0; Mismatches 340; Indels 9; Gaps 1;

Qy 1522 GGGTGTGAACCATGAGACCTGGTGTGGGTGAGCAGATTGGACGGGGAACTTTGGCG 1581
Db 1967 GGGAGCTTGATCCAGCGTGGCTGATGGTGACACTGTCTAGAGAGAGAGTTGGGG 2026
Qy 1582 AAGTGTTCAGCGGAGCTGGAGCC-----GACAACACCTGGTGGCGGTGAAGT 1632
Db 2027 AAGTGTATCGAGGAGACCTCAGGCTCCCGAGGAGCTGCAAGACTGTGGCCATTAA 2086
Qy 1633 CTTCGAGAGACCTCCACCTCAGGCTCAAGGCAAGTTTCTACAGAGAGCGAGGATCC 1692
Db 2087 CCTTAAAGACACATCCCGAGTGGCAGTGGTGGAACTTCTTCGAGAGCAACTATCA 2146
Qy 1693 TGAAGCAGTACAGCCACCCCAACATCGTGGTCTCATTTGGTGTCTGCACCCAGAGCAGC 1752
Db 2147 TGGGCCAGTTTAGCCACCCCGCATATTTCTGCATCTGGAAGGCGTCTGCACAAAGCGAAGC 2206
Qy 1753 CCATCTACATCGTATGAGAGCTTGTGCAGGGGGGCGACTTCTGAGACTTCTCCCGCAGCG 1812
Db 2327 TGAACCTACCTCAGTAATCACAATTTATGTCCACCGGACCTGGCTGCCAGAAACATCTGG 2386
Qy 1933 TGACAGAGAAGTGTCTGAGATCAGTACTTTGGATGTCCCGAGAGAGCCCGATG 1992

Db 2387 TGAATCAAAACCTGTCTGCTCAAGGTGTCTGACTTTGGCCTGACTCGCTCTCTGGATGACT 2446
Qy 1993 GGGTCTATGACAGCTCAGGGGGCTTCAGACAAAGTCCCGTGAAGTGGACCGCACCTGAGG 2052
Db 2447 TTGATGGCACATACGAAACCCAGGGAGGAAAGATCCCTATCCGTGTGACAGCCCTGAAG 2506
Qy 2053 CCCTTAACCTACGGCGCTACTCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTGTCTCT 2112
Db 2507 CCATTGCCCATCGGATCTTACCACAGCCAGCGATGTGTGAGCTTTGGGATTTGTGATGT 2566
Qy 2113 GGGAGACCTTTCAGCCTGGGGCTCTCCCTATCCAACTCAGCAATCAGACACACGGG 2172
Db 2567 GGGAGGTGTGAGCTTTGGGACAAAGCTTATGGGAGATGAGCAATCAGAGGTTATGA 2626
Qy 2173 AGTTTGTGGAGAAAGGGGGCGCTCTGCCCTGCCAGAGCTGTGTCTGTGATGCCGTGTTC 2232
Db 2627 AGAGCATTTAGGATGGTACCGGTTGCCCTCTCTGTGGACTGCCCTGCCCTCTGTATG 2686
Qy 2233 GGCTCATGAGCAGTCTGGGCTATGAGCCTGGGAGCGGCCAGCTTC 2282
Db 2687 AGCTCATGAAGAACTCTGGGCATATGACCGTCCCGCGGCCACACTTC 2736

RESULT 15

US-10-210-120-19
; Sequence 19, Application US/10210120
; Publication No. US20030175736A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Rubin, Mark A.
; APPLICANT: Sreekumar, Arun
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: UM-07221
; CURRENT APPLICATION NUMBER: US/10/210,120
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 3370
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-19

Query Match 7.4%; Score 198; DB 16; Length 3370;
Best Local Similarity 54.7%; Pred. No. 2.2e-21;
Matches 421; Conservative 0; Mismatches 340; Indels 9; Gaps 1;

Qy 1522 GGGTGTGAACCATGAGACCTGGTGTGGGTGAGCAGATTGGACGGGGAACTTTGGCG 1581
Db 1967 GGGAGCTTGATCCAGCGTGGCTGATGGTGACACTGTCTAGAGAGAGAGTTGGGG 2026
Qy 1582 AAGTGTTCAGCGGAGCCCTGGAGCC-----GACAACACCTGGTGGCGGTGAAGT 1632
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Qy 1693 TGAAGCAGTACAGCCACCCCAACATCGTGGTCTCATTTGGTGTCTGCACCCAGAGCAGC 1752
Db 2147 TGGGCCAGTTTAGCCACCCCGCATATTTCTGCATCTGGAAGGCGTCTGCACAAAGCGAAGC 2206
Qy 1753 CCATCTACATCGTATGAGAGCTTGTGCAGGGGGGCGACTTCTGAGACTTCTCCCGCAGCG 1812
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Wed Aug 10 16:17:22 2005

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Qy	1873	TGGAGTACCTGGAGAGCAAGTGTGTCATCCACCGGACCTGGCTGCTCGAACTGCCTGG	1932
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Qy	1933	TGACAGAGAAAGATGTCCTGAAGATCAGTGAATTTGGGATGTCCCGAGAGGAGCGGATG	1992
Db	2387	TGAATCAAAACCTGTGTGTCGCAAGGTGTCTGACTTTGGCCTGACTCGCCTCCTGGATGACT	2446
Qy	1993	GGGTCTATGAGCCTCAGGGGGCTCAGACAACTCCCGTGAAGTGGACCGCACCTGAGG	2052
Db	2447	TTGATGGCACATACGAACCCAGGGAGAAAGATCCCTATCCGTTGACAGCCCTGAAG	2506
Qy	2053	CCCTTAACTACGGCCGCTACTCTCCGAAAGCGACGTGTGGAGCTTTGGCATCTTGCTCT	2112
Db	2507	CCATTGCCCATCGGATCTTCAACACAGCCAGCGATGTGTGGAGCTTTGGGATTGTGATGT	2566
Qy	2113	GGGAGACCTTCAGCCTGGGGCTCCCTTATCCCAACCTCAGCAATCAGCAGACACGGG	2172
Db	2567	GGGAGGTGCTGAGCTTTGGGACAAAGCCTTATGGGGAGATGAGCAATCAGGAGGTATGA	2626
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Qy	2233	GGCTCATGGAGCAGTGTGGGCTTATGAGCCTGGGCGAGCGGCCAGCTTC	2282
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Job time : 2389.73 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2005, 16:42:25 ; Search time 591.209 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2674	100.0	2674	3	US-09-817-180-1
2	2674	100.0	2674	4	US-10-003-295-1
3	362.4	13.6	15297	3	US-09-817-180-3
4	362.4	13.6	15297	4	US-10-003-295-3
5	296.2	11.1	361	3	US-09-387-212-5
6	296.2	11.1	361	3	US-09-948-802-5
7	223.4	8.4	19152	4	US-09-949-016-12110
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9	198	7.4	3370	4	US-09-814-915A-82
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12	174.6	6.5	3386	4	US-09-949-016-5662
13	174.6	6.5	3416	2	US-08-357-642A-2
14	174.6	6.5	3416	2	US-08-460-626-2
15	174.6	6.5	3416	4	US-09-016-434-1483
16	174.6	6.5	4089	4	US-09-300-958A-13
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33	165.8	6.2	1521	2	US-08-604-989A-10	Sequence 10, Appl
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43	162.6	6.1	1548	3	US-09-099-053-1	Sequence 1, Appli
44	162.2	6.1	2440	1	US-08-160-861-2	Sequence 2, Appli
45	162.2	6.1	2442	1	US-08-542-363-3	Sequence 3, Appli

ALIGNMENTS

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; Sequence 1, Application US/09817180
; Patent No. 6340584
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO01183
; CURRENT APPLICATION NUMBER: US/09/817,180
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2674
; TYPE: DNA
; ORGANISM: Human
US-09-817-180-1

Query Match	100.0%;	Score 2674;	DB 3;	Length 2674;
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				0; Gaps
0;				
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Qy 2641 AAA 2674
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RESULT 2

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; Sequence 1, Application US/10003295
; Patent No. 6886187
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183DIV
; CURRENT APPLICATION NUMBER: US/10/003.295
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-003-295-1

Query Match 100.0%; Score 2674; DB 4; Length 2674;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1741 CCCAGAGCAGCCATCTACATCTCTCATGGAGCTTGTGAGGGGGGAGCTTCTGACCT 1800
Db 1741 CCCAGAGCAGCCATCTACATCTCTCATGGAGCTTGTGAGGGGGGAGCTTCTGACCT 1800
Qy 1801 TCCTCCGACAGAGGGGGCCCGCTCGGGGTGAAGACTCTGTGTCAGATGTTGGGGATG 1860
Db 1801 TCCTCCGACAGAGGGGGCCCGCTCGGGGTGAAGACTCTGTGTCAGATGTTGGGGATG 1860
Qy 1861 CAGCTGTGGATGAGTACCTGAGAGCAAGTGTGATCCACCGGAGCTTGTGCTC 1920
Db 1861 CAGCTGTGGATGAGTACCTGAGAGCAAGTGTGATCCACCGGAGCTTGTGCTC 1920
Qy 1921 GGAATGCTGTCACAGAGAAATCTCTGAGATCAGTGAATCTTGGATGTCCTCCGAG 1980
Db 1921 GGAATGCTGTCACAGAGAAATCTCTGAGATCAGTGAATCTTGGATGTCCTCCGAG 1980
Qy 1981 AGGAAGCCGATGGGCTCTATGAGCCTCAGGGGCTCAGACAAAGTCCCGTGAAGTGA 2040
Db 1981 AGGAAGCCGATGGGCTCTATGAGCCTCAGGGGCTCAGACAAAGTCCCGTGAAGTGA 2040
Qy 2041 CCGCAGCTGAGGCTTAACTACCGGCGCTACTCTCCGAAAGCGAGCTGTGAGCTTTG 2100
Db 2041 CCGCAGCTGAGGCTTAACTACCGGCGCTACTCTCCGAAAGCGAGCTGTGAGCTTTG 2100
Qy 2101 GCATCTTGTCTGGGAGACCTTCAGCCTGGGGGCTCCCGCTATCCCACTCAGCAATC 2160
Db 2101 GCATCTTGTCTGGGAGACCTTCAGCCTGGGGGCTCCCGCTATCCCACTCAGCAATC 2160
Qy 2161 AGCAGACCGGGATTTGTGAGAGAGGGGGCGCTGTGCGCTGCCAGAGCTGTGCTG 2220
Db 2161 AGCAGACCGGGATTTGTGAGAGAGGGGGCGCTGTGCGCTGCCAGAGCTGTGCTG 2220
Qy 2221 ATGCGGTTCAGCTCATGAGCAGTGTGGGCTATGAGCTTGGGAGCGGCCAGCT 2280
Db 2221 ATGCGGTTCAGCTCATGAGCAGTGTGGGCTATGAGCTTGGGAGCGGCCAGCT 2280
Qy 2281 TCAGCACCATTACAGGAGCTGCAGACATCCGAAAGGGGATCCGTCAGGCTGGGACC 2340
Db 2281 TCAGCACCATTACAGGAGCTGCAGACATCCGAAAGGGGATCCGTCAGGCTGGGACC 2340
Qy 2341 CCCTTTCAGAGCTGTGGCTCTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTG 2400
Db 2341 CCCTTTCAGAGCTGTGGCTCTGAGGCTTGTGAGGCTTGTGAGGCTTGTGAGGCTTGTG 2400
Qy 2401 TATGCTGACAGCTTTCACAGTCTCTGAGCTTGTGAGCTTGTGAGCTTGTGAGCTTGTG 2460
Db 2401 TATGCTGACAGCTTTCACAGTCTCTGAGCTTGTGAGCTTGTGAGCTTGTGAGCTTGTG 2460
Qy 2461 ATGAGCGGCTGTCTCTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2520
Db 2461 ATGAGCGGCTGTCTCTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2520
Qy 2521 AACATTAACCACTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 2580
Db 2521 AACATTAACCACTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 2580
Qy 2581 AA 2640
Db 2581 AA 2640
Qy 2641 AA 2674
Db 2641 AA 2674

RESULT 3

US-09-817-180-3

; Sequence 3, Application US/09817180

; Patent No. 6340584

; GENERAL INFORMATION:

; APPLICANT: GAN, Weinui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001183
; CURRENT APPLICATION NUMBER: US/09/817,180
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15297
; TYPE: DNA
; ORGANISM: Human
; US-09-817-180-3

Query Match 13.6%; Score 362.4; DB 3; Length 15297;

Best Local Similarity 99.7%; Pred. No. 5.1e-55;

Matches 363; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2187 GGGGGCGCTGCTGCCCTGCCAGAGCTGTGCTGATGCCGTTCAGGCTCATGGAGCAG 2246
Db 12938 GGGGGCGCTGCTGCCCTGCCAGAGCTGTGCTGATGCCGTTCAGGCTCATGGAGCAG 12997
Qy 2247 TCCTGGCCCTATGAGCTTGGGAGCGGCCAGCTTACCAACCATCTACAGAGCTGCAG 2306
Db 12998 TCCTGGCCCTATGAGCTTGGGAGCGGCCAGCTTACCAACCATCTACAGAGCTGCAG 13057
Qy 2307 AGCATCCGAAAGCGGATCGGTGAGCTGGGAGCCCTTCTCAAGTGTGGCTTGTGCA 2366
Db 13058 AGCATCCGAAAGCGGATCGGTGAGCTGGGAGCCCTTCTCAAGTGTGGCTTGTGCA 13117
Qy 2367 GGCCTAGGTGAGCTTCCAGCGGCTCCAGCTCATATGTCAGACCTTTCACAGTCCCTG 2426
Db 13118 GGCCTAGGTGAGCTTCCAGCGGCTCCAGCTCATATGTCAGACCTTTCACAGTCCCTG 13177
Qy 2427 GACTCCTGCCACAGCATCCACACTGCCGAGGATGAGCGCCGTGCTCTCTGTGTC 2486
Db 13178 GACTCCTGCCACAGCATCCACACTGCCGAGGATGAGCGCCGTGCTCTCTGTGTC 13237
Qy 2487 CCTGCTGTGCCAGGCTTCCCTTCCGGGAGAGAAATAAACCACTTGTGCCACTG 2546
Db 13238 CCTGCTGTGCCAGGCTTCCCTTCCGGGAGAGAAATAAACCACTTGTGCCACTG 13297
Qy 2547 AAAA 2550
Db 13298 AACA 13301

RESULT 4

US-10-003-295-3

; Sequence 3, Application US/10003295

; Patent No. 6686187

; GENERAL INFORMATION:

; APPLICANT: GAN, Weinui et al.

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; FILE REFERENCE: CL001183DIV

; CURRENT APPLICATION NUMBER: US/10/003,295

; CURRENT FILING DATE: 2001-12-06

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 15297

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-10-003-295-3

Query Match

13.6%; Score 362.4; DB 4; Length 15297;

Best Local Similarity 99.7%; Pred. No. 5.1e-55;

Matches 363; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2187 GGGGGCGCTGCTGCCCTGCCAGAGCTGTGCTGATGCCGTTCAGGCTCATGGAGCAG 2246

Db 12938 GGGGGCGTCTGCCCTGCCAGAGCTGTCTCTGATGCCGTTCAGGCTCATGGAGCAG 12997
Qy 2247 TGCTGGCCCTATGAGCTGGGCGAGCGGCCAGCTTACAGACCATCTACAGAGAGCTGCAG 2306
Db 12998 TGCTGGCCCTATGAGCTGGGCGAGCGGCCAGCTTACAGACCATCTACAGAGAGCTGCAG 13057
Qy 2307 AGCATCCGAAGCGGCATCGGTGAGCTGGGAGCCCTTCTCAAGCTGTGGCTCTGC 2366
Db 13058 AGCATCCGAAGCGGCATCGGTGAGCTGGGAGCCCTTCTCAAGCTGTGGCTCTGC 13117
Qy 2367 GGCCTAGGTGAGCTCTCAGCGGCTCCAGCTCATATGCTGAGAGCTTTCAGAGTCCCTG 2426
Db 13118 GGCCTAGGTGAGCTCTCAGCGGCTCCAGCTCATATGCTGAGAGCTTTCAGAGTCCCTG 13177
Qy 2427 GACTCTCTGCCACAGCATCACACTGCCGCGAGGATGCAGCGCGTGTCTCTCTGTGTC 2486
Db 13178 GACTCTCTGCCACAGCATCACACTGCCGCGAGGATGCAGCGCGTGTCTCTCTGTGTC 13237
Qy 2487 CTGCTGCTGCCAGGGCTTCTCTTCCGGGCGAGAAACATATAAACAATTTGCCCCACTG 2546
Db 13238 CTGCTGCTGCCAGGGCTTCTCTTCCGGGCGAGAAACATATAAACAATTTGCCCCACTG 13297
Qy 2547 AAAA 2550
Db 13298 AAAA 13301

RESULT 5
US-09-387-212-5
; Sequence 5, Application US/09387212A
; Patent No. 6309849
; GENERAL INFORMATION:
; APPLICANT: ROBISON, KEITH E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; FILE REFERENCE: MNI-090
; CURRENT APPLICATION NUMBER: US/09/387,212A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: All occurrences of n indicate any nucleotide
US-09-387-212-5

Query Match 11.1%; Score 296.2; DB 3; Length 361;
Best Local Similarity 97.4%; Pred. No. 1.1e-43;
Matches 333; Conservative 0; Mismatches 4; Indels 5; Gaps 3;
Qy 1684 CGAGGATCTGAAGCAGTACAGCCACCCCAACATCGTGGCTCTCATTTGGTGTGCACCC 1743
Db 20 CNAGGATCTGAAGCAGTACAGCCACCCCAACATCGTGGCTCTCATTTGGTGTGCACCC 79
Qy 1744 AGAAGCAGCCCATCTACATCGTGGGCGAGCAAGTGTGCATCCACCGGACCTGGTGTCCGA 1803
Db 80 AGAAGCAGCCCATCTACATCGTGGGCGAGCAAGTGTGCATCCACCGGACCTGGTGTCCGA 139
Qy 1804 TCCGACGAGGGGGCCCGCTGCGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAG 1863
Db 140 TCCGACGAGGGGGCCCGCTGCGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAG 199
Qy 1864 CTGCTGGCATGAGTACCTTGGAGAGCAAGTGTGCATCCACCGGACCTGGTGTCCGA 1923
Db 200 CTGCTGGCATGAGTACCTTGGAGAGCAAGTGTGCATCCACCGGACCTGGTGTCCGA 259
Qy 1924 ACTGCTGTGACAGAGAAAGATGTCTTGAAG-ATCAGTCACTTT-GGGATGTCCCGAGA 1981
Db 260 ACTGCTGTGACAGAGAAAGATGTCTTGAAG-ATCAGTCACTTT-GGGATGTCCCGAGA 319

Qy 1982 GGAAGCC---GATGGGTCTATGAGCCTCAGGGGGCCTCAG 2020
Db 320 GGAAGCCCGATTGGGGGTCTATGAGCCTCAGGGGGCCTCAG 361
RESULT 6
US-09-948-802-5
; Sequence 5, Application US/09948802
; Patent No. 6465232
; GENERAL INFORMATION:
; APPLICANT: ROBISON, KEITH E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; FILE REFERENCE: MNI-090
; CURRENT APPLICATION NUMBER: US/09/948,802
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 09/387,212
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 361
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: All occurrences of n indicate any nucleotide
US-09-948-802-5

Query Match 11.1%; Score 296.2; DB 3; Length 361;
Best Local Similarity 97.4%; Pred. No. 1.1e-43;
Matches 333; Conservative 0; Mismatches 4; Indels 5; Gaps 3;
Qy 1684 CGAGGATCTGAAGCAGTACAGCCACCCCAACATCGTGGCTCTCATTTGGTGTGCACCC 1743
Db 20 CNAGGATCTGAAGCAGTACAGCCACCCCAACATCGTGGCTCTCATTTGGTGTGCACCC 79
Qy 1744 AGAAGCAGCCCATCTACATCGTGGGCGAGCTTGTGCAGGGGGCGACTTCTTGAACCTTC 1803
Db 80 AGAAGCAGCCCATCTACATCGTGGGCGAGCTTGTGCAGGGGGCGACTTCTTGAACCTTC 139
Qy 1804 TCCGACGAGGGGGCCCGCTGCGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAG 1863
Db 140 TCCGACGAGGGGGCCCGCTGCGGTGAAGACTCTGCTGCAGATGGTGGGGGATGCAG 199
Qy 1864 CTGCTGGCATGAGTACCTTGGAGAGCAAGTGTGCATCCACCGGACCTGGTGTCCGA 1923
Db 200 CTGCTGGCATGAGTACCTTGGAGAGCAAGTGTGCATCCACCGGACCTGGTGTCCGA 259
Qy 1924 ACTGCTGTGACAGAGAAAGATGTCTTGAAG-ATCAGTCACTTT-GGGATGTCCCGAGA 1981
Db 260 ACTGCTGTGACAGAGAAAGATGTCTTGAAG-ATCAGTCACTTT-GGGATGTCCCGAGA 319
Qy 1982 GGAAGCC---GATGGGTCTATGAGCCTCAGGGGGCCTCAG 2020
Db 320 GGAAGCCCGATTGGGGGTCTATGAGCCTCAGGGGGCCTCAG 361

RESULT 7
US-09-949-016-12110
; Sequence 12110, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12110
; LENGTH: 19152
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12110

Query Match
Best Local Similarity 8.4%; Score 223.4; DB 4; Length 19152;
Matches 224; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 60 CGAACAGACATATGGGCTTCTTCTGAGCTGTGACGCCCGCCAGGGCCAGGGGTCCTG 119
DB 18729 CAGAACAGACATATGGGCTTCTTCTGAGCTGTGACGCCCGCCAGGGCCAGGGGTCCTG 18788
QY 120 CAGCAAAATGCAAGGCGGAGCTTCTTCTACTGAGGGCATGAGAAAGTGATGGCCAG 179
DB 18789 CAGCAAAATGCAAGGCGGAGCTTCTTCTACTGAGGGCATGAGAAAGTGATGGCCAG 18848
QY 180 CGGTCAGAGTGACAGGAGTATGACGAGCTGTTCACACATGTCCTCGCAGGACAGT 239
DB 18849 CGGTCAGAGTGACAGGAGTATGACGAGCTGTTCACACATGTCCTCGCAGGACAGT 18908
QY 240 GGGGCCAGAGCCGGGCCATCAGCCCTGACAGCCCCATCAGTCAG 284
DB 18909 GGGGCCAGAGCCGGGCCATCAGCCCTGACAGCCCCATCAGTCAG 18953

RESULT 8

US-09-949-016-15795
; Sequence 15795, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15795
; LENGTH: 19153
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15795

Query Match
Best Local Similarity 8.4%; Score 223.4; DB 4; Length 19153;
Matches 224; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 60 CGAACAGACATATGGGCTTCTTCTGAGCTGTGACGCCCGCCAGGGCCAGGGGTCCTG 119
DB 18729 CAGAACAGACATATGGGCTTCTTCTGAGCTGTGACGCCCGCCAGGGCCAGGGGTCCTG 18788
QY 120 CAGCAAAATGCAAGGCGGAGCTTCTTCTACTGAGGGCATGAGAAAGTGATGGCCAG 179
DB 18789 CAGCAAAATGCAAGGCGGAGCTTCTTCTACTGAGGGCATGAGAAAGTGATGGCCAG 18848
QY 180 CGGTCAGAGTGACAGGAGTATGACGAGCTGTTCACACATGTCCTCGCAGGACAGT 239
DB 18849 CGGTCAGAGTGACAGGAGTATGACGAGCTGTTCACACATGTCCTCGCAGGACAGT 18908
QY 240 GGGGCCAGAGCCGGGCCATCAGCCCTGACAGCCCCATCAGTCAG 284
DB 18909 GGGGCCAGAGCCGGGCCATCAGCCCTGACAGCCCCATCAGTCAG 18953

Db 18909 GGGGGCCAGAGCCGGGCCATCAGCCCTGACAGCCCCATCAGTCAG 18953

RESULT 9

US-09-814-915A-82
; Sequence 82, Application US/09814915A
; Patent No. 6750015
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Kathryn
; APPLICANT: Richer, Jennifer
; TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Related
; TITLE OF INVENTION: There to

; FILE REFERENCE: 2848-39
; CURRENT APPLICATION NUMBER: US/09/814,915A
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 60/214,870
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 82

; LENGTH: 3370
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-915A-82

Query Match
Best Local Similarity 7.4%; Score 198; DB 4; Length 3370;
Matches 421; Conservative 0; Mismatches 340; Indels 9; Gaps 1;

QY 1522 GGGTCTGAACCATGAGGACCTGGTGGTGGAGCAGATTGGACGGGGGAACTTTGGCG 1581
DB 1967 GGGAGCTTGATCCAGCGTGGCTGATGGTGGACACTGTCTAGGAGAAAGAGTTTGGGG 2026
QY 1582 AAGTGTTCAGCGGAGCGCTCGAGGCC-----GACAAACACCTGTGTGCGGTGAAGT 1632
DB 2027 AAGTGTATCGAGGGACCTCAGGCTCCCGACGAGGACTGCAAGACTGTGSCCAATGA 2086
QY 1633 CTGTGCGAGAGACGCTCCACCTCAGCTCAAGGCCAAGTTTCTACAGGAAGCGAGTCC 1692
DB 2087 CTTAAAGACACATCCCGAGTGGCAGTGTGGAACTTCCTTCGAGAGGCAACTATCA 2146
QY 1693 TGAAGCAGTACAGCACCCCAACATCGTGTCTCTATTGGTGTCTGCACCCAGAAAGCAGC 1752
DB 2147 TGGGCCAGTTTAGCCACCCGCAATTTCTGCACTCTGGAAGCGCTGTCACAAAGCGAAGC 2206
QY 1753 CCATCTACATCGTCATGAGCTTGTGAGGGGGGCGACTTCTTGACCTTCTCGGCAAG 1812
DB 2207 CGATCATGATCATCAGAAATTTATGGAGAAATGCGAGCCCTGGATGCTTCTCGAGGAGC 2266
QY 1813 AGGGGGCCCGCTGCGGGGTGAAGACTCTGCTGAGAGATGTTGGGGGATGCGAGCTGCTGCGCA 1872
DB 2267 GGGAGGACCAGCTGGTCCCTGGGCGAGTAGTGCCCATGCTGCGAGGGCATAGCATCTGGCA 2326
QY 1873 TGGAGTACCTGGAGAGCAAGTGTGATCCACCGGACCTGGCTGTCTCGGAACCTGCTCGG 1932
DB 2327 TGAACCTACCTCAGTAATACAAATTTATGTCACCGGACCTGGCTGCGAGAAACATCTTG 2386
QY 1933 TGACAGAGAAAGATGCTCTGAAGATCAGTGACTTTGGGATGTTCCCGAGAGGAAAGCGATG 1992
DB 2387 TGAATCAAAACCTGTGTCAGAGTGTCTGACTTTGGCCCTGACTCGCCCTCTCGATGACT 2446
QY 1993 GGGTCTATGAGCCTCAGGGGGCTCAGACAAAGTCCCGTGAAGTGGACCGCACCTTGAGG 2052
DB 2447 TTGATGGCAGATACGAAACCCAGGGAGGAAAGATCCCTATCCGTGGACAGCCCTTGAAG 2506
QY 2053 CCCTTAACCTACGCGCGCTACTCTCCGAAAGCGACGTGTGGAGCTTTGGGATCTTCTGCTCT 2112
DB 2507 CCAATGCCCATCGGATCTTCCACAGCAGCGAGTGTGTGGAGCTTTGGGATTTGTATGT 2566
QY 2113 GGGAGACCTTTCAGCTTGGGGGCTTCCCGCTATCCCAACCTCAGCAATCAGCAGACAGCGG 2172
DB 2567 GGGAGGTGCTGAGCTTTGGGGCAAGCCCTTATGGGGAGATGAGCAATCAGGAGGTTATGA 2626

Db 2457 CGTGGACCCCGCGAGGCGCATTTCTACCGGAAGTTACCTCTGCCAGCAGCTGTGG 2516
Qy 2094 AGCTTTGGCATTTGCTCTGGGACCTTCAGCCTGGGGCCTCCCTTATCCCACTTC 2153
Db 2517 AGCTTTGGCATTTGCTCTGGGAGGTGATACCTATGGCGAGGGCCCTACTGGGAGTTG 2576
Qy 2154 AGCAATCAGCAGACACGGGAGTTTGTGGAGAGGGGGCGTCTGCCCTGCCAGAGCTG 2213
Db 2577 TCCAAACACAGAGGTGATGAAGCATCAATGATGGCTTCGGCTCCCAACCCATGGAC 2636
Qy 2214 TGTCTCTGATCCCTGTCTAGGCTCATGGAGCAGTGTGGGCTATGAGCCTGGGAGCGG 2273
Db 2637 TGCCCTCCGCCATCTACAGCTCATGATGCAAGTGTGGCAGCAGGAGCGTGCCTGCCG 2696
Qy 2274 CCAGCTTCAGCACCATCTACAGGAGCTGCAGAGCATC 2312
Db 2697 CCCAAGTTGGCTGACATCTCAGCATCTCTGGACAAGCTC 2735

RESULT 12
US-09-949-016-5662
; Sequence 5662, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5662
; LENGTH: 3386
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5662

Query Match
Best Local Similarity 54.7%; Pred. No. 7.1e-22;
Matches 392; Conservative 0; Mismatches 319; Indels 6; Gaps 2;
Qy 1569 GGGAACTTTGGCGAAGTGTTCAGCGGACGCTCGAGCCGCAACACCTGGTGGCGGTG 1628
Db 1386 GGGAGGTCTATGAAGTGTCTACAAATCAAAAGGGGAGAAAATCAATGATGCTGTC 1445
Qy 1629 AAGTCTTGTGAGAGACGCTCCACCTGACCTCAAGGCCAAGTTTCTACAGGAAGCGAGG 1688
Db 1446 AAGACCTGCAAGAAAGACTGCACTCTGGACACACAGGAGAGTTTATGAGGAGCGAGTG 1505
Qy 1689 ATCTTAAGCAGTACAGCACCACCAACATCGTGTCTCTATGTTGTGACCCAGAG 1748
Db 1506 ATCATGAGAACTCGACCCACCGCACATCTGGAAGCTGATCGGCAT---CATTGAAGAG 1562
Qy 1749 CAGCCCATCTACATCGTCTATGGAGCTTGTGACGGGGGCGACTTCTGACCTTCTCCG 1808
Db 1563 GAGCCACCTGGATCATCATGGAATTTGATCCCTATGGGAGCTGGGCCACTACCTGGAG 1622
Qy 1809 ACGGAGGGGGCCCTGGGGTGAAGACTCTGTCTGACAGATGTTGGGGGATGCACTGCT 1868
Db 1623 CGAACAAGAACTCCCTGAAGGTGCTACCCCTGCTGTACTCACTGCAGATATGCAA 1682
Qy 1869 GCATGGAGTACTTGGAGCAAGTGTGATCCACCGGACCTGGTCTCGGAAGTGC 1928
Db 1683 GCCATGGCTACCTGGAGAGATCACTGCTGACAGGAGATTTGCTCCGGAACATC 1742
Qy 1929 CTGGTGACAGAGAGATGTCCTGAAGATCAGTGAATTTGGGATGTCCTCCGAGGAGGCC 1988

Db 1743 CTGTGGCCTCCCTGAGTGTGGAAGCTGGGGGACTTTTGGTCTTCCCGTACATTGAG 1802
Qy 1989 GATGGGTCTATGAGCCTTCAGGGGGCCTCAGAAAGTCCCGTGAAGTGGACCGACCT 2048
Db 1803 GACGAGGACTAT---TACAAAGCCTCTGTGACTCGTCTCCCATCAATGGATGTCCCCA 1859
Qy 2049 GAGGCCCTTAACCTACGGCGCTACTCTCGAAAGCAGCGTGTGGAGCTTTGGCATTTG 2108
Db 1860 GAGTCATTAATCTCCGAGCTTCACGACAGCAGGAGTGTGATGTTGCGCGTGTGC 1919
Qy 2109 CTCTGGAGACCTTCAGCCTGGGGGCTCCCTATATCCCACTCAGCAATCAGCAGACA 2168
Db 1920 ATGTGGAGATCTGAGCTTTGGGAAGCAGCCCTCTTCTGGCTGGAGAACAGGATGTC 1979
Qy 2169 CGGAGCTTTGTGGAGAGGGGGCGTGTGCGCTGCCAGAGCTGTGCTGATGCCGTG 2228
Db 1980 ATCGGGTCTGGAGAAAGGAGACCGGCTGCCAAGCCTGATCTCTGTCACCGTCTT 2039
Qy 2229 TTAGGCTCATGAGCAGTGTCTGGGCTTATGAGCCTGGCAGCGGCCAGCTTACG 2285
Db 2040 TATACCTCATGACCCGCTGCTGGACTACGACCCAGTACGACCGGCCCGCTTACC 2096

RESULT 13
US-08-357-642A-2
; Sequence 2, Application US/08357642A
; Patent No. 5837524
; GENERAL INFORMATION:
; APPLICANT: Sima Lev
; TITLE OF INVENTION: Joseph Schlessinger
; TITLE OF INVENTION: PYK2 RELATED PRODUCTS
; TITLE OF INVENTION: AND METHODS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/357,642A
; FILING DATE: December 15, 1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/070
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3416
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic
US-08-357-642A-2

Query Match
6.5%; Score 174.6; DB 2; Length 3416;

Best Local Similarity 54.7%; Pred. No. 7.1e-22;
Matches 392; Conservative 0; Mismatches 319; Indels 6; Gaps 2;
1569 GGGAACTTTGGCGAAGTGTTCAGCGAGCGCTCGGAGCCGACAAACACCTCTGGTGGCGGTG 1628
1416 GGGAGGTCTATGAAGTGTCTACACAAATCACAAAGGGGAGAAATCAATGTAGCTGTC 1475
1629 AAGTCTTGTGAGAGAGCTCCACCTGACCTCAGGCCAAGTTTCTACAGGAAGCGAGG 1688
1476 AAGACCTGCAAGAAGACTGCACCTCGGACAAAGAGGAAGTTTCATGAGCGGCGAGTG 1535
1689 ATCTGAAGCAGTACACCCACCCCAACATCGTGGTCTCATTTGTGTCTGCACCCAGAAG 1748
1536 ATCATGAAGAACCTGAGACCCGACATCGTAGCTGTATCGCAT---CATTGAAGAG 1592
1749 CAGCCCATCTACATCGTCTGAGAGCTTGTGAGGGGGGCGACTTCTTGACCTTCTCCCGC 1808
1593 GAGCCCACTGGATCATCATGGAATTTGTATCCCTATGAGGAGCTGGGCCACTACTCTGGAG 1652
1809 ACGAGGGGGCCCGCTCGGGGTGAAGACTCTGCTGAGATGGTGGGGGATGAGCTGCT 1688
1653 CGGAACAAGAACTCCCTGGAAGTGTCTCACCCTCGTGTCTACTCACTGCAGATATGCAAA 1712
1869 GGCATGAGTACCTGGAGAGCAAGTGTCTGATCCACCGGAGCTGGCTGCTCGGAATGC 1928
1713 GGCATGGCCCTACCTGGAGAGCATCAACTGGGTGCACAGGGAGCATTTGCTGCCGGAACATC 1772
1929 CTGGTACAGAGAAGAAATCTCTGAAGATCAGTACTTTGGGATGTCCCGAGAGGAAGCC 1988
1773 CTGGTGGCCCTCCCTGAGTGTGTAAGCTGGGGAGCTTTGGTCTTCCCGGTACATTGAG 1832
1989 GATGGGTCTATGAGCGCTCAGGGGGCTCAGACAAAGTCCCGTGAAGTGGACCGCACT 2048
1833 GAGCAGGACTAT---TACAAAGCCCTGTGTACTGTCTGCCCATCAATGGATGTCCCA 1889
2049 GAGGCCCTTAACCTACGGCCCTACTCTCCGAAGAGCACTGTGGAGCTTTGGCATCTTG 2108
1890 GAGTCCATTAACCTTCCAGCCCTTACAGACAGCAGTGTGATGTTTGGCGGTGTC 1949
2109 CTCTGGAGACCTTACGCTGGGGGCTCCCGCTATCCCAACCTCAGCAATCAGCAGACA 2168
1950 ATGTGGAGTGTGGAGAAAGAGACCGGCTGCCAAGCTGATCTCTGCCACCGGTCTT 2069
2229 TTAGGCTCATGAGCAGTGTCTGGGCTATGAGCTGGGCGAGCGGCCACCTTCAGC 2285
2070 TATACCTCATGACCCGCTCTGGGACTACGACCCAGTACCGGGCCCGCTTTCACC 2126

RESULT 14

US-08-460-626-2

; Sequence 2, Application US/08460626

; Patent No. 5837815

; GENERAL INFORMATION:

; APPLICANT: SIMA LEV

; APPLICANT: JOSEPH SCHLESSINGER

; TITLE OF INVENTION: PYK-2 RELATED PRODUCTS AND

; TITLE OF INVENTION: METHODS

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,626
FILING DATE: June 2, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/357,642
FILING DATE: December 15, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 211/121
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3416
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-460-626-2

Query Match 6.5%; Score 174.6; DB 2; Length 3416;
Best Local Similarity 54.7%; Pred. No. 7.1e-22;
Matches 392; Conservative 0; Mismatches 319; Indels 6; Gaps 2;

QY 1569 GGGAACTTTGGCGAAGTGTTCAGCGAGCGCTCGGAGCCGACAAACACCTCTGGTGGCGGTG 1628
DB 1416 GGGAGGTCTATGAAGTGTCTACACAAATCACAAAGGGGAGAAATCAATGTAGCTGTC 1475
QY 1629 AAGTCTTGTGAGAGAGCTGCCACCTGACCTCAAGCCAAAGTTTCTACAGGAAGCGAGG 1688
DB 1476 AAGACCTGCAAGAAGACTGCATCTGGAACAAAGAGGAAGTTTCATGAGCGGCGAGTG 1535
QY 1689 ATCTGAAGCAGTACAGCCACCCCAACATCGTGGTCTCATTTGTGTCTGCACCCAGAAG 1748
DB 1536 ATCATGAAGAACCTCGACCCACCGCACATCGTGAAGCTGATCGCAT---CATTGAAGAG 1592
QY 1749 CAGCCCATCTACATCGTCTGAGAGCTTGTGAGGGGGGCGACTTCTTGACCTTCTCCCGC 1808
DB 1593 GAGCCCACTGGATCATCATGGAATTTGTATCCCTATGAGGAGCTGGGCCACTACTCTGGAG 1652
QY 1809 ACGAGGGGGCCCGCTCGGGGTGAAGACTCTGCTGCAGATGTTGGGGATGAGCTGCT 1868
DB 1653 CGGAACAAGAACTCCCTGGAAGTGTCTACCCCTGCTGCTACTCACTGCAGATATGCAAA 1712
QY 1869 GGCATGAGTACCTGGAGAGCAAGTGTCTGCATCCACCGGAGCTGGCTGCTCGGAACTGC 1928
DB 1713 GGCATGGCCCTACCTGGAGAGCATCAACTGGGTGCACAGGGAGCATTTGCTGCCGGAACATC 1772
QY 1929 CTGGTACAGAGAAGAAATGTCTGGAAGATCAGTACTTTGGGATGTCCCGAGAGGAAGCC 1988
DB 1773 CTGGTGGCCCTCCCGTGAAGTGTGGAAGCTGGGGGACTTTGGTCTTCCCGGTACATTGAG 1832
QY 1989 GATGGGGTCTATGACAGCTCAGGGGGCTCAGACAAAGTCCCGTGAAGTGGACCGCACCT 2048
DB 1833 GAGCAGGACTAT---TACAAAGCCCTCTGTGACTGTCTCCCATCAATGAAGATGTCCCA 1889
QY 2049 GAGGCCCTTTAACTACCGCCGCTACTCTCCGAAGAGCAGTGTGGAGCTTTGGCATCTTG 2108
DB 1890 GAGTCCATTAACCTTCCAGCCCTTACAGACAGCAGTGTGATGTTTGGCGGTGTC 1949
QY 2109 CTCTGGAGACCTTACGCTGGGGGCTCCCGCTATCCCAACCTCAGCAATCAGCAGACA 2168
DB 1950 ATGTGGAGTGTGGAGAAAGAGACCGGCTGCCAAGCTGATCTCTGCCACCGGTCTT 2069
QY 2229 TTAGGCTCATGAGCAGTGTCTGGGCTATGAGCTGGGCGAGCGGCCACCTTCAGC 2285
DB 2070 TATACCTCATGACCCGCTCTGGGACTACGACCCAGTACCGGGCCCGCTTTCACC 2126

QY 2229 TTACAGGCTCATGAGCAGTGTCTGGGCTATGAGCCTGGGAGCGGCCAGCTTCAGC 2285
Db 2070 TATACCTCATGACCCGCTGCTGGGACTACGACCCAGTACCGGCCCCGCTTCACC 2126

RESULT 15

US-09-016-434-1483
; Sequence 1483, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1483:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3416 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9988304

US-09-016-434-1483

Query Match 6.5%; Score 174.6; DB 4; Length 3416;
Best Local Similarity 54.7%; Pred. No. 7.1e-22;
Matches 392; Conservative 0; Mismatches 319; Indels 6; Gaps 2;

QY 1569 GGGAACTTTGGGGAAGTGTTCAGCGGACGCTTCAGCGCGGACCAACACCCCTGGTGGCGGTG 1628
Db 1416 GGGAGGCTATGAGGTGTCTACACAATACAAAGGGGAGAAATCAATGATGCTGTC 1475
QY 1629 AAGTCTTGTGAGAGACGCTCCACCTGACCTCAAGCGCAAGTTTCTACAGGAAGCGAGG 1688
Db 1476 AAGACCTGCAAGAAAGACTGCACTCTGGACAACAAGGAGAAGTTTCATGAGCGAGGCAGTG 1535
QY 1689 ATCTGTAAGCAGTACAGCCACCCACACATCGTCGCTCATTTGGTGTCTGACCCAGAG 1748
Db 1536 ATCATGAAGAACTTGACCCCGGACATCGTGAAGCTGATCGCAT--CATTTGAAGAG 1592
QY 1749 CAGCCCATCTACATCGTCAATGGAGCTTGTGACAGGGGGGCGACTTCCTGACCTTCCTCCGC 1808
Db 1593 GAGCCACCTGATCATCATGGAATTGTATCCCTATGGGAGCTGGGCCACTACCTGGAG 1652

QY 1809 ACGAGGGGGCCCGCTGCGGGTGAAGACTCTGCTGCAGATGTTGGGGATGACAGTGTCT 1868
Db 1653 CGGAACAAGAACTCCCTGAAGGTGCTCACCCCTGCTGTACTCACTGCAGATATCAAA 1712
QY 1869 GGCATGGAGTACCTGGAGAGCAAGTCTGCATCCACCGGACCTGCTGCTCGGAATGTC 1928
Db 1713 GGCATGGCTTACCTGGAGAGCATCAACTCGTGCACAGGAGCATTTGCTGTCGGAACATC 1772
QY 1929 CTGGTGACAGAGAAGAAATGTCTCTGAAGATCAGTGACTTTTGGGATGTCCCGAGAGGAAGCC 1988
Db 1773 CTGGTGGCCTCCCTGAGTGTGTGAAGCTGGGGGACTTTGGTCTTTCCCGGTACATTGAG 1832
QY 1989 GATGGGCTCTATGCAGCCTCAGGGGCTTCAGACAAGTCCCGTGAAGTGGACCGCACCT 2048
Db 1833 GACGAGGACTAT---TACAAAGCCTCTGTGACTCGTCTCCCATCAAAATGGATGTCCCA 1889
QY 2049 GAGGCCCTTAAGTACGGCGCTACTCCTCCGAAAGGAGCTGTGGAGCTTTGGCATCTTG 2108
Db 1890 GAGTCAATTAACTTCGAGCCTTCAGGACGACGAGTGTGATGTTCCCGGTGTC 1949
QY 2109 CTCTGGGAGACCTTCAGCCTGGGGCCTCCCTATCCCAACCTCAGCAATCAGCAGACA 2168
Db 1950 ATGTGGAGATCCTGAGCTTTGGGAAGCAGCCCTTCTTCTGGCTGGAGAAACAAGATGTC 2009
QY 2169 CGGGAGTTTGTGAGAGAGGGGGCGCTGTGCTGCTGCCAGAGCTGTGCTGATGCCGTG 2228
Db 2010 ATCGGGGTGCTGGAGAAAGGAGACCGGCTGCCCAAGCCTGATCTCTGTCACCGGTCCTT 2069
QY 2229 TTACAGGCTCATGGAGCAGTGTGGGCTTATGAGCCTGGGAGCGGCCAGCTTCAGC 2285
Db 2070 TATACCTCATGACCCGCTGCTGGGACTACGACCCAGTGGACCGGCCCGGCTTCACC 2126

Search completed: August 9, 2005, 21:35:02
Job time : 595.209 secs